

APPROVED	O. FIG.
BY	
DRAFTSMAN	
	CLASS      SUBCLASS

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA  
 CCCACCGCGTCCGGGCCGGAGCAGCACGCCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG  
 CAGCGCTACCCGCCATGCGCCTGCCGCCGGCCGCTGGGCTCCTGCCGTTCTGCTG  
 CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT  
 GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAACTTGGCCGGGGAAACA  
 CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC  
 CTGGAGGGCTGTGCGAGAGCAGCGACTCGAATGCAATCAGATGCTAGAGCGCAGGAGGA  
 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT  
 GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC  
 CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA  
 GGGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG  
 ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
 TGCAAGACGTGCTGGCCTGACCAACAGAGACTGCCGAGTGTGAAGTGGCTGGTGCT  
 GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
 CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG  
 GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA  
 CGGACAGTGTGAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGTGAGGAAAAACG  
 AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAAACG  
 GAAGATGCCGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
 GCCCTCCCGCAAGACCTGTAATGTGCCGACTTACCCTTAAATTATTAGAAGGATGTCC  
 CGTGGAAAATGTGCCCTGAGGATGCCGCTCCTGCAGTGGACAGCGGCCGGAGAGGCTGC  
 CTGCTCTCTAACGGTTGATTCTCATTGTCCTAAACAGCTGCATTCTTGGTTGTTCTTA  
 AACAGACTTGTATTTGATAACAGTTCTTGTAATAAAATTGACCTTGTAGGTAATCAGG  
 AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC  
 TTGGCCGCCATGGCCAACCTGTTATGCAAGCTTATAATGGTTACAAATAAGCAATAGCA  
 TCACAAATTTCACAAATAAGCATTTCCTACTGCATTCTAGTTGTGGTTGTCACAAACTC  
 ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTGCCGCGACGACCATGGCCTGAAAT  
 AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCCGGAAAGAACCAAGCTGTGGAATG  
 TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCGAGCAGGCAGAAGTATGCAAGCATGC  
 ATCTCAATTAGTCAGCAACCCAGTTT

## **FIGURE 2**

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLPPAPEAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIR  
LLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPC  
SGNGHCSGDGRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEGVWV  
LDEGACVDVDECAAEP PCSAAQFCKNANGSYTCEEC DSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC  
AEKTCVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

**Signal peptide:**

amino acids 1-24

**N-glycosylation sites.**

amino acids 190-194 and 251-255

**Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

**Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299,  
339-343 and 349-353

**Tyrosine kinase phosphorylation site.**

amino acids 303-310

**N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258  
and 313-319

**Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

**EGF-like domain cysteine pattern signature.**

amino acids 166-178

**Leucine zipper pattern.**

amino acids 94-116

## **FIGURE 3**

CAGGTCCAAC TGAC CCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTGCGTAGGTGCG  
GCACGAGGAGTTTCCCAGCGAGCAGGAGGTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCCTGGCACTGCCGGCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGTCACCAGGCAAGAGTACTCA  
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT  
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCGTGCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGGAACAGTGCCTCACAGGCA  
TCAGTTGTTCAAGTTGGTTCCCATGTCTGGAAAACAGGATGGGTTGGCAGCATTGAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTAAACATGTCAACAAAGCTGAGTGCCTCAGGCCGGTGGCAAATGGAGGCTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG  
TACCCCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTCTGCATCTGCCAACCTG  
GATTCTATGGAGTGAACGTGACAAAGCAAACGTCAACCACCTGCTTTAATGGAGGGACC  
TGTTCACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCACAACCCCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT  
CCAAAGGTTACCAAGGGAGACCTCTGTTCAAAGCCTGTCTGCAGCCTGGCTGGTGCACAT  
GGAACCTGCCATGAACCCAAACATGCCATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCAGCTCAGGCAGC  
ACACGCCCTCACTAAAAAGGCCAGGGAGCAGGCCAGCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCCTTGTAAACCTTCA  
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGGCCTGAATTATTAGCT  
TCATTATAAATCACTGAGCTGATATTACTCTCCCTTTAAGTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTCTGTTCAGTGTCTGGCAGATATTCAAATTACAATGCATTATGGT  
TCAGGTTAAAATTTCAGTGTAGTTGGCAGATATTCAAATTACAATGCATTATGGT  
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTATTGTCAAGATATTAGAT  
GTTTGTACATTAAAATTGCTCTTAATTCAAATTCTCAATACAATATAATTGACC  
TTACCAATTCCAGAGATTCACTGAGGTTAAATTACACTGTGGTAGGGCATT  
AAACAATATAATATTCTAAACACAATGAAATAGGAAATAATGTATGAACATTGCA  
TGGCTGAAGCAATATAATATTGTAAACAAAACACAGCTCTTACCTAATAAACATT  
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGGAAAAAAA  
AAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTGGC  
GCCATGGCCCAACTGTTATTGCAGCTTATAATG

## FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094

><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVP  
LGVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGG  
RNNGFCNERRICECPDGFHGPCHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANC  
STTCFNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKICIGSKCKCSKGYQGDLC  
SCKPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

**Signal peptide:**

amino acids 1-28

**N-glycosylation site.**

amino acids 88-92, 245-249

**Casein kinase II phosphorylation site.**

amino acids 319-323

**Tyrosine kinase phosphorylation site.**

amino acids 370-378

**N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

**EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## **FIGURE 5**

CGGACGCGTGGCGTCCGGCGGTGCAGAGCCAGGAGGCGGAGGCAGCGCGGGCCAGCCTGGG  
CCCCAGCCCACACCTCACCAAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGCTAC  
TGCTGTTGCTGCCGCTGGCCTGGCCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG  
GAGCTAGCACCGGTCTGCACCTGCAGGGCATCCGGACGCAGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGCCGTGCCAGCAGACTGTGCCCTGCCACTCTGGCGCCATCT  
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCAGCTGCTGCCCTGACTCTGGGACTTC  
TGCCTCGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTGGAACGTACTGGGACAAGTGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCATTCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTCTGGGCATGACCTGGATGAGGCATTGCTACCGCCTGGCACCA  
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGTGAACCCAGGGAG  
GTGCTTCCCACAGCCTCGAGGCCTCTGAGAAGTGGCCAACCTGATTATGAGCCTCTGA  
CCAAGGCAACTGTGAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCCTGTCCTGCCCCAGAACCTGCTGTCTTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGCGTCTGATGGTGCCTGGTGGTCCTGCGTCG  
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGGAGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCAGGCCATGGTCGGGCAAGCGCAGGCCACTGCC  
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGGCC  
CAGCCTGGGGCAGAGGGCCACTTCCGATCGTGCAGGGCTCAATGAGTGCACATCGAG  
AGCTTCTGCTGGCGTCTGGGCCGCGTGGGCATGGAGGACATGGTCATCACTGAGGCTG  
CGGGCACCAAGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCGGCCAGAGGCCCAATG  
GGCGGTGACCCAGCCTCGCCGACAGAGGCCGGCGCAGGCGGCCAGGGCGCTAAT  
CCCGCGCGGGTCCGCTGACGCAGGCCCGCTGGGAGGCCGCCAGGGCGAGACTGGCG  
GAGCCCCAGACCTCCCAGTGGGACGGGCAGGGCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGGCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATAACCCACCCAAATCCGTATTCTTTTTTTAGACAGGGTCTGCTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACCTCCACTCCTGGGTTCA  
AGTGCACCTCCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCAACACCTGGC  
TAATTTTGTTGAAAGAGGGGGTCTCACTGTTGCCAGGCTGGTTGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGCTGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAAA  
AAAAACCAAAGTATTGATAAAAAAA

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209,  
296-300, 411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

## **FIGURE 7**

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTCTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG  
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

## **FIGURE 8**

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGCCACTCCTCACAGACCTG  
GCCCAAGTGGGAGCCTGTCCCTGGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCTCTGCTGCTGTTTC  
CATGGCCCAGCATTCTCACCCCTTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT  
CCCTGCCACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGACCCAGCA  
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTCCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALR  
RAQ

**Signal peptide:**

amino acids 1-47

**N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

**Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

**N-myristoylation site.**

amino acids 56-60

**Amidation site.**

amino acids 70-74

## **FIGURE 10**

CCACACCGTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC  
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCAGCAGGAAAGACAAAGACTG  
CGTGTTCACGGAGATCGTGTGGAGAACAACTATACGGCCTCCAGAACGCCGGCAGGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGCGGCCCGCCAGGCTCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACCACGC  
CGAGAACGAGCAGCTCGAGTTGTGGCTCCGCCACCGCCGGACCAAGCGCACAC  
GGCGGCCAGCCCTACGTAGTCTGGAGGCAGGGGGCAGCAGGCCCTGGCCGCCTCCC  
CACCCCTTCCCTTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC  
GAGGGAGGACCTGAGGCCCGAAGCATCCGAGCCCCCAGCTGGGAAGGGCAGGCCGGTG  
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAACCT  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGCTCCTGAAGCC  
CGCTGAAAGGTAGCGACTGAAGGCCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGCCCCAACTCCTCTGGCTAGACTGTA  
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCCAACTCCCAGCCC  
CGGAATAAAACCATTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI  
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRKGKLGKPSGSKDCVFTEIVLE  
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF  
VGSAPTRRTKRTRRPQPLT

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 9-13, 126-130

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

**Casein kinase II phosphorylation site.**

amino acids 65-69

**Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

**N-myristoylation site.**

amino acids 69-75, 188-194

**Amidation site.**

amino acids 58-62

**HBGF/FGF family signature.**

amino acids 103-128

## **FIGURE 12**

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCAGATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC  
CATACGCCCTCAGGACGTCCCTCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT  
CATTTGATTTGCTGTTATTTTTCTTTCTTTCCACCACATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTCCT  
GAAGTCTTGGCTATCATTCCTGGGCTCTACTCACAGGTGTCCAAACTCCTGGCTGCC  
CTAGTGTGTGCCGCTGCACAGGAACTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG  
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAAATTAAATGC  
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATCCCCATGAACCTCCAAAGAATGTCAGAGTTCTCCATTGAGGAAAAC  
AAATATTCAAGACCATTCACGGCTGCTCTGCCAGCTTGAAGCTGAAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTGCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA  
TCTCACCGAGCTGGAGCGCTTTATTGTGGACGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC  
CACCCCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGAGGACAACCAGAT  
AAACCACATTCCCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTGGTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCAACGTGCGGGGTTCATGTGCCAAGGTCTGAACAAGTCCGGG  
GGATGGCGTCAGGAATTAAATATGAATCTTGTCCCTGCTCCACGACCCCCGGCCTG  
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCACTCAGCCTCCCACCCCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCCTCAAACCTTACACATCGAAACTTCCCACGATT  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCTCTATC  
CATTTGTGAATGATACTCCATTCAAGTCAGCTGGCTCTCTCTTCAACCGTGTGGCATA  
CAAACTCACATGGGTGAAAATGGCCACAGTTAGTAGGGGCATCGTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGTTTAACCTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC  
CACCAACCATGCCCTCATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTTGATGGGGCGCGGTGATATT  
GTGCTGGTGGCTTGCTCAGCGTCTTGTGCTGGCATATGCACAAAAGGGCGCTACACCTC  
CCAGAAGTGGAAATACAACCGGGCGGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCTGGAGATGACAGAAACAGTTCAAGTCTCCTAAATAACGAT  
CAACTCCTAAAGGAGATTCAGACTGCAGCCCATTACACCCAAATGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC  
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTCACATAAAGACACGAGATTACATTGATAATGTTACACAGATGCAT  
TTGTGCATTGAAACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG  
CTATCTTCTATTCAAGTTAACAGTTGTAACCTTTGCTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPShGAFFLKS~~W~~LIISLGLYSQVS~~K~~LLACPSVCRCDRNFVYC~~N~~ERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHQENNIQTI  
SRAALAQLLKLEELHLD~~D~~NSISTVGVEDGAFREAI~~S~~LKLLFLSKNH~~S~~SPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDG~~N~~LLTNKGIAEGTF~~S~~HLTKLKEFSIVRNSLSH~~PP~~PD  
LPG~~T~~HLIRLYLQDNQINH~~I~~PLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN~~N~~  
PWFCD~~C~~SIK~~W~~VT~~E~~WLKYIPSSLNV~~R~~GFMCQGPEQVRGM~~A~~VRELNM~~N~~LLSCPTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSY~~T~~PPPTSKLPTIPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWL~~S~~LFTVMAYKLTWV~~K~~M~~G~~H~~S~~L~~V~~GGIVQERIVSGEKQHLSLVNLEPRSTYR~~I~~CLVPL  
DAFNYRAVEDTICSEATTHASYLNN~~G~~NTASSHEQTTSHSMGSPF~~L~~LAGLIGGA~~V~~IFV~~V~~V~~L~~  
LSVFCWHMHKKGRYTSQ~~K~~W~~K~~YNR~~R~~R~~K~~DDYCEAGT~~K~~K~~D~~NSILEMTETSFQIVSLNN~~D~~QL~~K~~KG  
DFRLQPIYTPN~~G~~GINYTD~~C~~H~~I~~PNMRYCNSSVPDLEH~~C~~HT

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 542-561

**N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639,  
649-653

**Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602,  
651-655

**Tyrosine kinase phosphorylation site.**

amino acids 319-328

**N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

**Amidation site.**

amino acids 581-585

**Leucine zipper pattern.**

amino acids 164-186

**Phospholipase A2 aspartic acid active site.**

amino acids 39-50

## **FIGURE 14**

ACTTGGAGCAAGCGCGGGCGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCCTCCCACGAGC  
GATCCCCGAGGAGAGCGCGGGCCCTCGCGAGGCAGAGAGGCCAGGAGAAGACCCGGGTGGCTGCGCCCTG  
CCTCGCTTCCCAGGCAGGGCTGCAGCCTGCCCTCTTGCTCGCCCTGAAAATGAAAGATGCTCGCAG  
GCTGCTTCTGCTGATCCTCGACAGATCGCCTCTCCCTGCCAGGGCAGGGAGCGGTACGTGGAGGGTCC  
ATCTCTAGGGCAGACAGCTCGACCCACCGCAGACGCCCTCTGGAGAGTCTGTGAGAACAGCGGGC  
AGACCTGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATCG  
TGGACATCTTGCATTGGACATTGGCTGTGATGTCACCCAGTGGCTGCTCAATATGGCAGCACTGTC  
AAGAATGAGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGGTGGAGCGTGTCAAGAGGATGCGGCATCT  
GTCCACGGGACCATGACTGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGAGGGGCC  
GGCCCTGAGGGAGAATGTGCCACGGGTATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCGAG  
GTGGCTGTAAGGCACGGACACGGCATCCTAATTTGCCATTGGTGTGGCCAGGTAGACTCAACACCTT  
GAAGTCCATTGGAGTGGACATGAGGACCATGCTTCCCTGTGGCAATTTCAGCCAGATTGAGACGCTGA  
CCTCCGTGTTCCAGAAGAAGTGTGACGGCCACATGTGACGCCCTGGAGCATAACTGTGCCCACTCTGC  
ATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGCATACATTCTCAACTCGGATCAGACGACTTGCAG  
AATCCAGGATCTGTGTGCCATGGAGGACACAACACTGTGAGCAGCTGTGTGAATGTGCCGGCTCCTTGTCT  
GCCAGTGTACAGTGGCTACGGCTGGCTGAGGATGGGAAGAGGGTGTGGACTACTGTGCCCTCAGAA  
AACACCGATGTGAACATGAGTGTGAAATGCTGATGGCTCCATACCTTGCAGTGCCTGAGGATTGCTCT  
TAACCCAGATGAAAAAAACGTGACAAGGATCAACTACTGTGCACTGAACAAACCCGGCTGTGAGCATGAGTGC  
TCAACATGGAGGAGAGCTACTACTGCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCG  
CGAGTGGACCACTGTGCACAGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCTTGTCT  
CCAGTGTCAAGAGCTTCCATCAACAGGGACCTCAAGACCTGCTCCGGTGGATTACTGCTGAGTGC  
ACCATGGTTGTGAATACTCTGTGTCACATGGACAGATCCTTGCCTGTCAGTGTGAGGGACACGTGCTC  
CGCAGCGATGGAAAGACGTGCAAAATGGACTCTGTGCTGGGGACCACGGTTGTGAACATTGTGAGT  
AAGCAGTGAAGATTGTTGTGCAAGGTTATATACTCCGTGAAGATGGAAAAACCTGAGAA  
GGAAAGATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTGTGAAACAGTGCAGACTCATACAGTGC  
GAGTGTGGAGGGATTCCGGCTCGCTGAGGATGGGAAACGCTGCCAGGAAGGATGTCTGCAAATCAACCA  
CCATGGCTGCAACACATTGTGTTAATAATGGAAATTCTACATCTGAAATGCTCAGAGGGATTGTTCTAG  
CTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCAATTGACCTGGCTTGTGATCGATGGATCCAAG  
AGTCTTGGAGAAGAGAATTGAGGTCGTGAAGCAGTTGTCACTGGAATTATAGATTCTTGCACATTCCCC  
CAAAGCCCTCGAGTGGGCTGCTCCAGTATTCCACACAGGTCACACAGAGTCACTCTGAGAAACTTCAACT  
CAGCCAAAGACATGAAAAAGCCGTGGCCACATGAAATACATGGAAAGGGCTCTATGACTGGCTGGCCCTG  
AAACACATGTTGAGAGAAGTTTACCAAGGAGAAGGGCCAGGCCCTTCCACAAGGGTGCAGAGCAGC  
CATTGTGTCACCGACGGACGGCTCAGGATGACGTCTCGAGTGGGCCAGTAAAGCCAAGGCCATGGTATCA  
CTATGTATGCTGGGTAGGAAAAGCATTGAGGAGGAACACTACAAGAGATTGCTCTGAGCCACAAACAAG  
CATCTCTCTATGCCAAGACTTCAGCACAATGGATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTAAGC  
TCTAGAAGACTCCGATGGAAAGACAGGACTCTCCAGCAGGGAAACTGCCAAAAACGGTCAACAGCCACAGAAAT  
CTGAGGCCAGTCACCATAAATCTCAAGACCTACTTCTGTTCTAATTTCAGTGAACACAGATATCTGTT  
GAAGAAGACAATCTTACGGTCTACACAAAAGCTTCCATTCAACAAAACCTTCAGGAAGCCCTTGGAGA  
AAAACACGATCAATGCAAAATGTGAAAACCTTATAATGTTCCAGAACCTTGCAAACAGGAAGTAAGAAAATTAA  
CACAGCGCTTAGAAGAAATGACACAGAGAATGGAAAGCCCTGGAAAATGCCCTGAGATACAGATGAAGATTAGAA  
ATCGCGACACATTGTAGTCATTGATCACGGATTACAATGAACGCAGTGCAGAGGCCAAAGCTCAGGTATT  
GTTAAATCAATAATGTTGTGAAGTAAAACATCAGTACTGAGAACCTGGTTGCCACAGAACAAAGAACAGAA  
GTATACACTAATTGTATAAATTATCTAGGAAAAAAACCTTCAGAATTCTAAGATGAATTACCAAGGTGAGA  
ATGAATAAGCTATGCAAGGTATTTGTAATATACTGTGGACACAACCTGCTTCTGCCATCTGCCATTAGTGT  
GCAATCTCATTTGACTATACGATAAAGTTGCACAGTCTTACTCTGTAGAACACTGCCATAGGAAATGCTGT  
TTTTTGACTGGACTTACCTTGATATGTATATGGATGTATGCATAAAATCATAGGACATATGTACTTGTG  
GAACAAGTTGGATTTTTATACAATATTAACCACTTCAG

## FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFLKTFKRKSEVERAVKMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENPRVIMIVTDGRPQDSVAEVAAKARDTGILIFAI GVGQVDFNTLKSIGSEPHEDHVFVLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAE DGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGCEEHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCEHSCVSSEDSFVCQCFCFGYILREDGKTCRCKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRCKDVKSTHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKCTEGPIDLVFVIDGSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKAIEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS PAGELPKTVQQPTESEPVTINIQDLLCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPGSPL EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

**Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247, 401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784, 781-785, 819-823, 866-870

**N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500, 639-645, 690-696, 752-758, 792-798

**Amidation site.**

amino acids 314-318, 560-564, 601-605

**Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464, 540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTAGCGGCTGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGGGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC  
**CATGATTCCCTCCGGGCCCCCTGGTACCAACTTGCTGCGGTTTGTTCTGGGCTGA**  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTC  
ATCCCAGCCATGGGAGGTGCCCTTGTATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGTCACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC  
ATGCCCTCCCGAACCTGTCCTCGGGCTGGAGGGCTCCAGGAGAAAGACTCTGGCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGAAATCTAGGGCCACAGCATAAAACCT  
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG  
GGTCTTAAGCCTCACCAACCTTGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC  
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGCCCAAGAGCTCAGACACAATCTCCAAGAATGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**  
CCCACCACTCATGGCTAAAGGATTGGGTTCTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC  
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG  
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTGAGTCAGC  
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC  
TTATTAAAACATGAAATATGTGTTGTTCTTCAAATTTAAATAAGATAACATAA  
TGTTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVWMFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAAPRTLWPWPKSSDTISKNGTL  
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 245-267

**N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

**N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258,  
256-262, 262-268, 308-314, 363-369, 364-370

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## **FIGURE 18**

CGCCACCACTGCGGCCACGCCAATGAAACGCCTCCGCTCTAGTGGTTTTCCACTTTG  
TTGAATTGTTCTATACTCAAAATTGACCAAGACACCTGCTCTCCAAATGCAAATGTGA  
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAAGGAAATGGTGTACAA  
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGCCTGTGGCGAAAATGCTAATTGC  
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA  
AGACAGGTTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT  
TAGATAATGTCTGTATAGCTGCAAATATTAAATAAAACTTTAACAAAATCAGATCCATAAAA  
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA  
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTTACAAGAACAAACA  
CTATCTCAGCCAAGGACACCCCTTAACACTCAACTCTTACTGAATTGAAAAACCGTGAAT  
AATTGTTCAAAGGGATACATTGTAGTTGGGACAAGTTATCTGTGAATCATAGGAGAAC  
ACATCTTACAAAACATGACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC  
AAAAGACCACAGAGTTGATACAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT  
TCATATAACATGAAACATATTCTACCTCATATGAATATGGATGGAGACTACATAAATATATT  
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTGATTTTATATTATA  
AGAGTATTGGTCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT  
AATTCTGAAGAGGGAGGAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCC  
ACCCACATTATATGAACTTGAAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA  
GGTATAGGAGTCTATGTGCATTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT  
TCAGAGGGCTGTGAGCTGACACTCAAAATGAGACCCACACCTCATGCCGCTGTAATCACCT  
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTCT  
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTTCTGCCATATGCATT  
ACCTCTGGTCTCAGTGAATTCAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG  
TAGCCTATTCTGCTGAACCTGTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT  
TCTGTTCAATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC  
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTGCA  
CAAGAAATTATCTTGGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTCGGCAGCAC  
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCAGAAACTTTATT  
TGGAGTTTATAGGACCAGCATGCCAATCATTCTGTTAATCTCTGGCTTGGAGTCAT  
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC  
TAAGGTCTGTGCAAGAGGGAGCCCTCGCTCTGTTCTCGGCACCTGGATCTT  
GGGTTCTCCATGTTGCACGCATCAGGGTACAGCTTACACTCTCAGTCAGCAATGC  
TTTCCAGGGATGTTCAATTGTTTATTCTGTGTTTATCTAGAAAGATTCAAGAACAT  
ATTACAGATTGTTCAAATGTCCCCTGTTGTTGGATGTTAAGGTAAACATAGAACATG  
GTGGATAATTACAACGTGCACAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA  
TGACTCATCAAATTATCCAATTAAACTACTAGACAAAAGTATTAAATCAGTTTCT  
GTTTATGCTATAGGAACGTGAGATAATAAGGAAATTATGTATCATATAGATATACTATGT  
TTTCTATGTAAGGAAATAGTTCTGTCAAAATAGTATTGCAAGATATTGGAAAGTAATTGGTTT  
CTCAGGAGTGTATCACTGCACCCAAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA  
TGTCTGAGGAAACACTGGCTGATATTCTGTGACTCGTGTGCTTGGAAACTAGTCC  
CCTACCAACCTCGGTAAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGA  
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACTGTTTCTGTAGAC  
TAGCTGAGAACATTGTTGACATAAAATAAGAATTGAAGAACACATTACCAATTGAA  
TTGTTCTGAACTTAAATGTCCACTAAAACAACATTAGACTCTGTTGCTAAATCTGTTCTT  
TTTCTAATATTCTAAAAAAAAAAAGGTTACCTCCACAAATTGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCNTTEGSYYCMCVPGRSSNQDRFITNDGTVCIENVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEYRNSVTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTL  
SNSTLTFVKTVNPFVQRDTFVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSNGNVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDYRSLCAF  
WNYS PDTMNGWSSEGCELTYSNETHTSCRNCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAI CIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL  
LHYFFLAFAFWMCIEGIHYLIVVGVIYNKGFLHKNFYIFGYLSPA VVGFSAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593,  
619-636, 648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## • **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT  
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAAC TGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA  
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTGCAATTGATGTCCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

## **FIGURE 21**

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCCGCAGATCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA  
CAAGAACGCCGCCCTGCCTGCCCGGGCCGGGGAGGGGCTGGGCTGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG  
TGTCTGGGCACCTACCCGTGGGCCCGTAAGGCCTACTATATAAGGCTGCCGCCGGAG  
CCGCCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGCCACGACCATCCAAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCCGCCAGCCTCCGCACCCCCATGCCGG  
AGCTGCCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTCTCGGACGCCGG  
CCACGTGCACTACGGCTGGGCGACCCCCTCCGCCTGCCACCTGTACACCTCCGCC  
ACGGGCTCTCCAGCTGCTTCCTGCGCATCCGTGCCACGGCGTGTGGACTGCCGCC  
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTTGCGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCACGGCAAGATGCAGGCCGTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTCAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCCTACAGCGGCCAGCTGTACAAGAA  
CAGAGGCTTCTCCACTCTCTCATTCCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG  
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAGTAAC  
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGACG  
TGCTTCTACAAGAACAGTCCCTGAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA  
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGTTCTAGCCAATAGACTTGCTGAT  
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTTGAATACCTCCATCGATGGGAAC  
TCACCTCCTTGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTCACTCAACCCATGTGGATTGATCTATCTACTTCCAGGG  
ACCATTGCCCTCCAAATCCCTCAGGCCAGAACGTGACTGGAGCAGGCATGCCACCAG  
GCTTCAGGAGTAGGGAAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC  
CTGAGGCCAGTTCTGTCATGGATGCTGTCCCTGAGAATAACTGCTGTCCGGTGTACCTGC  
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTGTTAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAAAGCAGCGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA  
TCTCTTATTTCATTACATTATGCCCCAAATTATATTATGTATGTAAGTGGAGTTG  
TTTGTATATAAAATGGAGTTGTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## **FIGURE 23**

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGCCCAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA  
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTCGGAGTGTCTCCTTGTCTAC  
TATCAACAGACTCTCAAGGTATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGTGCGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATAACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGAAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC  
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCGCAATT  
TGTTGGATATCGCAGGTGCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA  
AGCCACGACAATGAGTAAAATGTGCAGTGGCTCACGCCGTAAATCCAGCACTTGGAAGG  
CCGCGGGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTGAACCCGGGAGGGGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAAATAAAATAATA  
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

## **FIGURE 24**

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT  
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEV  
SAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEY  
TWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN  
SVGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPVI  
PALWKAAGGSRGQ  
EF

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 130-144, 238-258

**N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

**Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

**N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

**Amidation site.**

amino acids 226-230

## **FIGURE 25**

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGCAACATTATTAACATGCTCACAGCCGGACCCTGGCAT  
CATGCTGCTATTCTGCAAATACTGAAGAACATGGATTAAATATTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTACATACACTCCACCTCAAAAAGTACATCAATA  
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCAATATGCATGACATTGGACATG  
CAATTGTGGCACTGGCACTTATTCTAGTGAAGAAAACCTTGTGGTTCTATGGCATTCA  
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACCTACTAGCACTGACTG  
TGGAACTCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAACATCAGGCCTGGTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTAACTTCCCAGCCAGATTGCC  
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATATTGCAAAATTAAGTACACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT  
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTTACTGA  
ACTGCCTGAAAATGTCGTCCGAACTGAGCAACTTACAAGAACTCTATATTAAATCACA  
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT  
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCTGGTT  
GGACTGAAAACCTAGAAAGCATCTTTACGATAACAGGCTTATTAAAGTACCCATGT  
TGCTCTCAAAAGTTGAAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAAGAGTTGGGATAAAATATGCCT  
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC  
TACTAACAAACCTAGATTGCTTACATTCAACCCAAATGCATTTCAGACTCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTCAGGCCAGATTCACTGTTGCGTGGACC  
CACCTGAATTCCAAGGTAGAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTG  
CTCCCTCTTATAGCTCCTGAGAGCTTCTAATCTAAATGTAGAAGCTGGAGCTATGT  
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG  
GTCAAAAACCTTGCTTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAATGGCGTACTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG  
GCTCTTGAATATTAAGAGATATTCAAGGCCATTCACTGTTGGTGTCTGGAAAGCA  
AGTTCTAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGTGCGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAACAGAAAAAAA  
TGTGTAAATGTACCACCAAGGTTGCACCCGTACAAAAAGAGTATGAAAAGAATAATAC  
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCCAGAAATGAACGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG  
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTACCAACAAATATGCTC  
AAAAACCAAGAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQILLQTNNAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRLVIAGINLTEIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVVNLKFLLDKNPKINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTIESLPNLKEISIHSNPIRC  
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNVQHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRAETAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTKGLHPDQKE  
YEKNNTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVATVIGLPTNMS

**Signal sequence:**

amino acids 1-22

**Transmembrane domain:**

amino acids 633-650

**N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526,  
579-583, 608-612, 624-628, 625-629

**Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

**Tyrosine kinase phosphorylation site.**

amino acids 570-579

**N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

**Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGGAGTAGATGAGGAATGGGCTCGTATTGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA  
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTCTCCTCTGGG  
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG  
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAAATGGCATTGAGTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGAAAACGTCCGTGGATGAACATGCTGGCAGACCATTCCAATGCTGC  
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTCACTATGGTATCTCATATGTGGTATTATGTGAGGAAAATCAGGAG  
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGAAACATTGAA  
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACTTAACAAACACTACAACA  
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT  
AATTAAAAGCAAATAAAAGCTTAACTTGAACCATGGGAAAAAAAAAAAAAAA  
ACA

## **FIGURE 28**

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF  
LNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK  
ADEPDDISTVV

**Signal sequence:**

amino acids 1-33

**Transmembrane domain:**

amino acids 205-220

**N-glycosylation site.**

amino acids 47-51, 94-98

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

**Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

**N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## **FIGURE 29**

ACCGAGCCGAGCGGACCGAAGGCGGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCATCCTCGCTGGTGC  
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCCTGCGAGTGCCTCGGCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCAGGGCATCCCCACCGAG  
ACGCGCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGGAGCGCCGTGGAGGCCAG  
CCTTCAACAACCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCTGAAGCTCATC  
CCGCTAGGCGTCTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
CGTTATCCTACTGGACTACATGTTAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCACCGGCCCTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT  
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC  
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCGCCACCTAGTCTATCTCGCTCCTCAACCTCTCCTACAACCCCATCA  
GCACCATGGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG  
GGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTCCACTCGGTGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCTGTGGTGTCCGG  
CGCCGCTGGCGCTCAACTCAACCGCAGCAGCCACGTGCGCACGCCAGTTGTCCA  
GGGCAAGGAGTTCAAGGACTCCCTGATGTGCTACTGCCAACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGAAGGCCAGCAGGTGTTGTGGACGAGGGCACACGGTGCAGTT  
GTGTGCCGGGCGATGGCGACCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCAGGTACAGGACAACGGCACGTACCTGCACTCGCGGCCAACCGGGCGCAACGAC  
TCCATGCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATGACCCAAACAA  
GACCTTCGCTTCATCTCCAACCAGCCGGGAGGGAGAGGCCAACAGCACCGGCCACTG  
TGCCTTCCCTCGACATCAAGACCCCTCATCATGCCACCACATGGCTCATCTCTTC  
CTGGCGCTGTCCTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC  
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCGCAAGTTAACATGAAGATGATATGAGGCCGGGCGGGGGCAGGGACCCCG  
GGCGGCCGGGAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCAGTCCTCCACCTC  
CTCCCTACCTTACACACGTTCTCTTCTCCCTCCGCTCCGCTCCCTGCTGCCCG  
CCAGCCCTCACCAACCTGCCCTCTACAGGACCTCAGAAGGCCAGACCTGGGACCCCA  
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC  
ATAATTCAATAAAAAGTTACGAACCTCTGTAACCTGGGTTCAATAATTATGGATTT  
TATGAAAATGAAATAATAAAAAGAGAAAAAAACTAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH  
WPYLDLMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRLVNVSGNQLTLEESVFHSVGNLETLILDSNPLA  
CDCRLLWVFRRLWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 556-578

**N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297,  
341-345, 492-496, 505-509, 526-530, 542-546

**Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352,  
349-353, 607-611

**Tyrosine kinase phosphorylation site.**

amino acids 590-598

**N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## **FIGURE 31**

CCCACCGGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC  
TGTTCGCCTGCTGCTGGCGCCCGGCGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGTGCTCAAGTGCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTTGGGAGAAGA  
GAGCCCTCGAGATAATCGAATTCAAGCTGGTACCTCTACGCCAACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCCATCATCACTGGTT  
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACACTCCACGGAGAACCAACCGCAT  
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGCGAGCATCGTGTGCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGCCAGAACAGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTC  
CCCAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA  
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTCCCT  
CCTCCTCCAGCACCTACCAACGCCATCATCGTGGGATCGTGGCTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCAGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGAGCACAAGAACGAAATTTCATCTAGAGGCCCTGCCACTTCCTGC  
GCCCCCAAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAACATGTCTGC  
TTGGGTGCGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA  
AACAAAAAACAA

## **FIGURE 32**

MGAPAASLLLLLFAACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISISNVALADEGEYTCISIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

**Signal sequence:**

amino acids 1-20

**Transmembrane domain:**

amino acids 331-352

**N-glycosylation site.**

amino acids 25-29, 290-294

**Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

**N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 33**

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCCTTCTCCTTCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGGCAGCAGGATGGTCGCTG  
TTACTTGTATGAGATCGGGATGAATTGCTCGCTTAAAAATGCTGCTTGGATTCTGTT  
GCTGGAGACGTCTTGTGAAACGTTACAGGGGACGTTGCAAAGAGAAGA  
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCATGGCAATT  
CCTCACTCGACTTTCCCTAATGAGTTGCTAATTATAATGCGTTAGTTGCACATGG  
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTCTGGGCTGCAGCTGGTGAAAAGG  
CTGCACATCAACACAACAAGATCAAGTCTTCTGAAAGCAGACTTTCTGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCCTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGGGAGATCCTCTAGAGGATAACCC  
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGCTTGGAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTGCTCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCCCTAGCTAAC  
GTTTACCTGCCCTGGGGCTGCAGCTGCACCACATCCAGGGTGGTTAAAGATGAAC  
TGCAACACAGGAACGTGAGCAGCTGGCTGATTGAAGCCAAGCTCTAACGTGCAGGA  
GCTTTCCCTACGAGATAACAAGATCCACAGCATCCGAAAATCGACTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGCAACAAATAACATCGTACTGTAGAGAACACACTTCAAG  
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA  
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATCTAACAAACACCTG  
CTGAGGTCCCTGCCGTGGACGTGTTGCTGGGCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACAGTTAACCTCCATCATCCAGA  
TAGACCTCACGGAAACCCCTGGAGTGCTGACAATTGTGCCTTCAAGCAGTGGCA  
GAACGCTTGGGTTCCGAAGTGTGATGAGCAGCTCAAGTGTGAGACGCCGGTGAACCTCTT  
TAGAAAGGATTTCATGCTCCTCTCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
GCCACGTTAACCTCGCACAGTAAAAACAGCACTGGGTTGGCGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCCAGCAGGGTGTCCATCTGGTGTGGTCCGGGACTGCTGTT  
GTTTGTACCTCCGCCTCACCGTGGCTGGCATGCTCGTGTGTTATCCTGAGGAACCGAAAGC  
GGTCCAAGAGAGCAGAGATGCCAACCTCCCGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GACTCTCCTACTGGCACAATGGGCCTTACAACGAGATGGGCCACAGAGTGTATGACTG  
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAAGGCG  
ATACATCCTCCCCACCGCAGGCAACCCGGGGCTGGAGGGCGTGACCCAAATCCCCGCG  
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA  
GCCAGCTCGCTCTTGCTGAGAGCCCTTGACAGAAAGCCAGCAGCACGCCCTGCTGGAG  
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCCTGTGGGTTGGATGCCCGGTTCTATAC  
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCTCTGTTGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGATGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAAATAAGTAACCTTGACTTCTGAC

## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLLNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLAPPAAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGLKMCNNRNVSSLADLK  
KLSNVQELFLRDNKIHSIRKSHFDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDICPQLYARISPLTSHSKNSTGLAETGTHNSYLDTSRVSISVL  
VPGLLLVFVTSAFTVVGMLVILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 618-638

**N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

**Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370,  
573-577, 608-612, 657-661, 666-670, 693-697

**N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## **FIGURE 35**

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTGTGCGGGCTAAGGGAAACTGTTGGC  
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGTCCGTCGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTCGCTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTCGTGCCTGGGGCCTCAG  
**AGAAT**GAGGCCGGCGTTGCCCTGTGCCTCCTCTGGCAGGGCCTCTGGCCCGGGCGG  
CGGCGAACACCCCCTGCGACCGTGTGCTCGGCCTCGGGGCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCAGGAGGAGGCCTGCATCCTGCAGGGGGCGCTC  
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCCTGTGCTCGCCTCGGGCAGGCCAGG  
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTCGCACTGGAGCGCAGGGCTCCACT  
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGCTCCGACCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGTGAGGCTGAGGAGATGCGATGCCACCTGC  
GCGCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTTGTGCTCGCCGCCCCGG  
GCCGCCTCTAACTTGAGCTATCGCGGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTGCA  
TCGCGGACGAAATCGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTCCTGCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTGGGAGG  
CTTGCCCTGCGAATGTGCTACGGGCTTCGAGCTGGGAAGGACGGCCGCTTGTGACCA  
GTGGGAAGGACAGCGACCCCTGGGGGACCGGGGTGCCACCAGCGCCGCCACT  
GCAACCAGCCCCGTGCCAGAGAACATGCCAATCAGGGTCGACGAGAACGCTGGGAGAGAC  
ACCACTGTCCCTGAACAAGACAATTCACTGAGTACATCTATTCCCTGAGATTCTCGATGGGAT  
CACAGAGCACGATGTCTACCCCTCAAATGCCCCCTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT  
CGACTCCTCCTGCGCTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT  
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGAACGCCCCCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCGCGGGCTGGAGAGTGTGATCTGAGCCCCTGCTTGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTGCTGGCGAGTCCCCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC  
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTTCTCAAATTCCCTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTGTG  
TGGTGTGATCTGGGGACCGGGTAGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA  
TTTGGAGAAGTGTGAACTTTCAAGACATTGAAACAAATAGAACACAATAATTACA  
TTAAAAAAATAATTCTACAAAATGGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT  
ATTGGTTGAAATCCCAGGGAAAAAATAAAAATAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALEERRSHCTLENEPLRGFSWLSSDPGGL  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPG  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVLVILMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDEPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 189-193, 381-385

**Glycosaminoglycan attachment site.**

amino acids 289-293

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

**Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

**N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

**Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGGCTGGGATTCAAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATGCCCTTAAAAGTGCCTCCGCCCTGCCGGCCGCTATC  
CCCCGGCTACCTGGGCCCGCCCCGGCGCGTGCAGCAGTGTGAGAGGGAGCGCGGGCAGCGA  
GCGCCGGTGTGAGCCAGCGCTGCCAGTGTGAGCGGCCGGTGTAGCGCGGTGGGTGCGGA  
GGGGCGTGTGCGCCGGCGCGCGCCGTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCCTGGCGCCACTCTGCCCTGCTGGCTGCCGCCACCCAGCTCTCGCG  
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTGGAAAATCA  
CAGTTCCCGAAGGAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGCCG  
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTTAAAC  
CCCCAAGTGGCCAGACCGGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGAACTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCA  
TTTATCAGACTTAAGTTAAGTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA  
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA  
ACCCACCGTGGCCTGTGTCACACAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGAATTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGAGTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCTCTCCTCAGAACAGGTC  
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGAAAATCATGCCAACAGC  
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCTGGATGCCCTTAAAGAATGCAATG  
TTAACAGTGAACGTGTCATTAAAGCTGTATTCTGCCATTGCCCTTGAAGAGTCTATGTT  
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCAGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTATTATACATCTGTAAAGGAT  
ATTTAGAATTGAGTTGTGAAGATGTCAAAAAAGATTTAGAAGTGCATATTATAGT  
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTGCCGTTCTA  
AATCAATGCTTAATAAAATTTTAAAGGAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVVLNFRFIDLESNDLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI  
QFLSDLSSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

**Signal sequence:**

amino acids 1-23

**N-glycosylation site.**

amino acids 355-359

**Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

**Tyrosine kinase phosphorylation site.**

amino acids 199-208

**N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

**Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGCGGACCGTGGCGGCCACGGCGCCGGCTGGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGAGGCCCCATGGCCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG  
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAACATTGTCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTCACAAAGCAGCAGGAGGCCCCGGACCTCTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC  
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAACCG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT  
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAACGG  
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTCTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGGACTTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGGAGGGCTCATCAAGGGCAGA  
TCGCGGCCACCACTGTAGGACCTCCCTCCCACCCACGCTGCCCGAGCTGGCTGCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCAGGTACCCAGGCCAGACAGAACGGCCCTGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCTGCCAGTTCTGT  
TCTGTGTTACCACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA  
AAGGTCTGGAAAGTAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 40**

MAPWPPKGVLPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLESELVESWWFHQK  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPGPGTERPCGGYQCEGEGRGGSGHCDCQAG  
YGGAEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKSPGYQQVGSKCLDVDECE  
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

**Signal sequence:**

amino acids 1-29

**Transmembrane domain:**

amino acids 372-395

**N-glycosylation site.**

amino acids 79-83, 205-209

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

**N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173,  
173-179, 177-183, 188-194, 250-256, 253-259, 267-273, 280-286,  
283-289, 326-332, 372-378, 395-401

**Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193

## **FIGURE 41**

TGAGACCCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTTGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGAGCTGCAGCTCAAAGAGGT  
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTACATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTAGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCTGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCCAGCTTCCAGG  
AGCCGGTCCCCAAGGCCGGCTGCACAGGCACGGCGGCTGTCCCCCGCGAGCGCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGCCGTGA  
CTCCAGGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCGGAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCGCTCGCAGGGGGC  
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGACTATGGAG  
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGGCCGGCTT  
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTCAAGTGGC  
CGTTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAACAGGAGGCCATAGGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG  
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA  
GAGCCCTGCTCAGTTCTATTCTATTACTGCACATATTCTAACGACTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCTGTCAC  
TGGATCTGGCTAAAGTCCCTCCACCACTCTGGACCTAACGACCTGGGTTAAGTGTGGGT  
TGTGCATCCCCATCCAGATAATAAGACTTGTAAAACATGAATAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFQSOFREVAGRFLALEASTHLLVFGMEQLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEHQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 158-162

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

**N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

**Amidation site.**

amino acids 74-78

**TGF-beta family signature.**

amino acids 282-298

## **FIGURE 43**

GTCTGTTCCCAGGAGTCCTCGCGCGTGTGTCAGTGGCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAGTTGACCA  
AGGAGACACCACCACTCGTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAAC TGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTTCTGAATAACACCTGGTTCAAAGAT  
GGGATAGTGTGATGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATAACTGGAGAATACA  
GCTGTGAGGCACCGAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGG  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGCTACCCCTGATGTCTGTAGTTCACAGGATGCC  
TACACCCACAGGGCCCCCTACTTCTCGATGTGTTTAATAATGTCAGCTATGTGCC  
ATCCTCCTTCATGCCCTCCCTCCCTTCCATACCACTGCTGAGTGGCCTGGAACCTGTTAAA  
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG  
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG  
CCACTGGATCCCTCTGCCCTGCTCTGAATACAAGCTGACTGACATTGACTGTCTGT  
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG  
GATTAAAACCGCTGCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC  
TAATCCCAGAGGCTGAGGCAGGCCATCACCTGAGGTGGAGTTGGATCAGCCTGACCA  
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS  
CAYSGFSSPRVEW  
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGT  
YTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI  
PSSATIGNRAV  
LTCSEQDG  
SPPSEYTWFKDGIVM  
PMTNP  
KSTRAFSNS  
SYVLNPTTGE  
LVFDPLSAS  
DTGEYSCEAR  
NGYGT  
PMTSNAVR  
MEAVERN  
VGVIVAAVL  
VTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSAR  
SEGEFKQTSSFLV

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 238-255

**N-glycosylation site.**

amino acids 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

**Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

**N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243,  
256-262

## **FIGURE 45**

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTCCACCCCGACCTCTGCCAGGCCAGGCCAGCTCAG  
GCTCGTCCCACCCACCAAGTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA  
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTGCTGGCTCCGAGCCAGGAGCGC  
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC  
CTCGCTGCCCTGAGGACAAGCAACTGCCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## FIGURE 46

MSGGWMAQVGAWRTGALGLALLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLD CSDGSDEEECRIEPCTQKGQCP PPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLA CLAGELRCTL SDDCIPLTWRCDGHPDCPDSDEL CGTNEILPEGDATTMGPV  
LESVTSLRNATTMGPVTL ESVP VGNATSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLG LLLVAMKESLLLSEQKTS LP

**Signal sequence:**

amino acids 1-30

**Transmembrane domain:**

amino acids 230-246

**N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

**Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

**N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172,  
212-218, 224-230, 230-236, 263-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

**Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCACACGGTCCGGTCTCGCTCGCGCAGCGGCGGAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGGAGGGAGGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTGCAAGCTGGATGCCCTCTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG  
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT  
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTCAGGACCCCCAGCG  
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCCTAGGCTGGATCCAAGTGA  
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTGTGATGAAGGATTCAAGATCCGG  
TACCCGACCTACACAATATGGTTCTATGTGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTAATGGCTATGTAACATCTGAGC  
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT  
GATGGGTCTCGTATCTTGAGTGCCTACAAAACCTTATCTGGCGTCCAGCCCACCCGGTG  
CCTTGCTCTGGAAGCCAAAGTCTGTCCACTACCTCCAATGGTAGTCACGGAGATTCGTCT  
GCCACCCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCCCTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG  
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTGGCATGCTCCGTCCTATG  
ACGAAGCTGTGAGTGGCGCTTGAGTGCCTAGGCCCGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTAACCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA  
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA  
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTTGGACAACCCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTGCTGAAGTGTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTGGTTTAGACAAATGTAACCAA  
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTGATCAAGTC  
CTGTTCTTCTGACACAGACTGATTAAAAATTAAAAGNAAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS  
VSGSELLQSLYSPPRCQESTHPASDNPDI IASTAEEVASTSPGIHHAHWVLFLRN

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 325-344

**N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

**Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

**N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## **FIGURE 49**

CCACCGGTCCGCCCTCCGCCCTCCCCCGCTCCCGTCCGGTCCGGTGGCTAGAGA  
TGCTGCTGCCGCCGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGGCCCTCCACCGCCGT  
AGCGCCCGAGTGTGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGTACAGG  
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCGACGGGTCGCCTGCTGAGTGCC  
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA  
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAGAACGCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT  
CACAATTAGGAACTGGTATGTGGATGAGCCGTCTGCCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGAATGATGA  
CCGGTGCAACATGAAGAACATTCATTGCAAATATTCTGATGAGAACACCAGCAGTTCCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG  
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCTGAATCTGCCCTACAT  
CTTAATCCCCAGCATTCCCTCTCCTCCTTGTGGTACCCACAGTTGTATGTTGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC  
TGGCCCTCTCCTCACCAAGGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAAATATTCAATTCCGAGTGTGTT  
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA  
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGAAAATGAAATATATG  
GTTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAATC  
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATCCTTAT  
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAATGTCACTTGGTGGTTATCTAACCTTAAGGGACAGAGCTTACCTG  
GCAGTGATAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTCTGCTATACAG  
CAGCACATATTACAGACAGAAAATCCAGAACATTCAAAGCCCACATATGGTAGCA  
CAG  
GTTGGCCTGTGCATCGGAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAGA  
GCAGGAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIFHDTSRRL  
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPyMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTPVLPEETQEEAKTFKESREAALNLAYILIPSIPLLLLLV  
VTTVVCWWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSQDQMGRSKES  
GWVENEIYGY

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 117-121, 312-316

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

**Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## **FIGURE 51**

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCCTGCAGCCTAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAAGCATGCGCTTGTGGACCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC  
GCTCCCCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAACTC  
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT  
GCAGCAAATGTTGCCTTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC  
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG  
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAAAGTCTTGTATCCAACTACCAAACCTGCTGGAGCCTGA  
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG  
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTGACCACAAATGCCACCGTTGCT  
GTTGACCTGACCATGAACTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT  
TCTTGAAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACGTATTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAAGTGCCTTATACAAATG

## **FIGURE 52**

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTOFDYTVNLAGGPKPYSFYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD  
FFIILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## **FIGURE 53**

CTCCTCTAACATACTTGCAGCTAAAACAAATATTGCTGCTGGGACCTCCTCTAGCCT  
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT  
GCCATTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACCGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCCCAGCTGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTGTATGCCACAGCAGAAAAAGAGCAAAAGGTCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG  
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGA  
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAACCAACCTCA  
GGATTGCCCTCTGGCCTGGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCG  
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTGTGATGACAACACTGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGCTGTGGAAAGTCCCTCTCCCTCAGAGACCGGA  
AATGCTATGCCCTGGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG  
CAGTCCCTGGAGCAGTGCAGCACAGATTGGGGTTCACTGACACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT  
TCTTCTGCCCTGGACTGGACTTAACTTGGTCCCCCTGATTCTCAGGCCTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTCTCAGGCCATCAGACATAGTTGGAAACTACATCA  
CCACCTTCCTATGTCTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTAT  
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGCTCTGGTAAAGAAGTCTGACAAAATACAGATTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTAAAGATAAATTCTGAATTGGTATGGGTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGLASPSGVRLVGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCAGASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTCQTGWSLRAAKVVCRLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSRLEVLIKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

**Signal sequence:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

**N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104,  
137-143, 180-186, 263-269, 286-292

**Amidation site.**

amino acids 196-200

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## **FIGURE 55**

ACTGCACTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACCGCGTCCGCGGACCGCGTGGCGGACCGCGTGGGCCGGTACCAAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCTGGG  
CGTCTCGGCCTTTCCGGCTGCTGCAGTGGTGCGCGGGAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTACCTCGACC  
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC  
GACATACTGTCAACAATGCTGGATCAGCTACCGTGGTACCATATGGACACACCACAGTGG  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA  
CTGTCTCGTGCCGAGATGAAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTGTAAATGCCATACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACACAGGCCAGGGCGAAGCCCTGTTGGAGGTGGCCAGGATGTTCTGCTGCTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTACTTACTGCCTTCCTGGCTGTTATCTCGAA  
CTCTGGCTCCTGGCTTTCAAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACCTCTAGACTCTGACCAGCCAGGGCAGAGAAGCAGCACTCTAGGCTTG  
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTAATGGAGATTGTCTACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGGCCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTGTTATTGCAGCTATAATGGTTA  
C

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLQQWVRGKAYLRNAVVIITGATSGLGKEAKVFYAAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI  
VAAAELQCFGYVDIL  
VNNAGISYRGTIMDTTDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVVAQDVLAAGKKKDVILADLLPSLAVYRLTLAPGLFFSLMASRARKERKSKNS

**Signal sequence:**

amino acids 1-21

**Transmembrane domain:**

amino acids 104-120, 278-292

**N-glycosylation site.**

amino acids 228-232

**Glycosaminoglycan attachment site.**

amino acids 47-51

**Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

**Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

**N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

**Amidation site.**

amino acids 265-269

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## FIGURE 57

CCCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAAAACGCTCGCAGCCACAAAAGGGGATGAAATTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCCCTAA  
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA  
GAATGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTCCAAGGTTCATACCTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA  
GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATTGTCACTGTGGCTCGGCAG  
CTGGACATGTCTCGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA  
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATACTGGAGTCAAAACAAACATG  
TCTGTGTCCTAATTGCTAAACACTGGCTCATCAAAATCCAAGTACAAGTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTAACAAACATTGAAAGGATCCTTCTGAGCGTT  
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAGCACCTAGTTCTGAAAATGATTACAGGTTAGGTTGATGTCATCTA  
ATAGTGCAGAATTAAATGTTGAACCTCTGTTTCTAATTATCCCCATTCTCAATA  
TCATTGGAGGCTTGGCAGTCTCATTTACTACCACTGTTCTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAAGGAAAATGAAGAAAAGAA  
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA  
AATTGTACCATAACGTTATTAAACATATATTATTGATTGCACTTAAATTGTT  
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCAAATAAAA  
TGAAGGACTATCTAGGGTATTCAACATGAAATCATGAACTCTCAATGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCCAATGCCAACATTCT  
GCACAGGGAGCTAGAGGTGGACACGTGTTGCAAGTATAAAAGCATCACACTGGATTAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA  
AA  
AA

## **FIGURE 58**

MKFLLDILLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

**Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

**N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216.

## **FIGURE 59**

CCACCGCGTCCGGACCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC  
AGGGAGGAGCACCGACTGCGCCGCCACCCCTGAGAGATGGTTGGTGCATGTGGAAGGTGATTG  
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTCGCTCCCTATACAGAAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTCGGCCCTTCCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC  
TTCCCAGCTCAGATAACGCCAGAACAGATGCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCTATGTTGTCACAAGTAACATGA  
CCTTGCGTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT  
AGCACGGGATTTATACAGTGCACTAATTCACTGTTCCAGATATTCCTGAATATAAAAATA  
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCATGAATGCATAGAACACATC  
AGGAAGCAGAACACTGGTTGAGGCCTTGAAACTGGATAAAACTACTAGATGGCGACTTAAC  
AAAGTATCCTTACTTCCAGAACATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT  
GCACGGAACCTGAGGATCAGTTACTATGAAATTTGCACTCCCAGAGGTGAGACAA  
GCCATCCACGTGGGAATCAGACTTTAATGATGAACTATAGTTGAAAAGTACTTGCAGA  
AGATAACAGTACAGTCAGTTAACGCATGGTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAACAGGAGAAAAAGTTGGAAGATCTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTACTTCCATCAGGTAAATTATC  
GAGGTGGAGGACATATTTACCTATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA  
TTCATTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCCAGAGAACAT  
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTCATATCTGCAAGATTTTTCATCAATAAAATTATCCTGAAACAAGTGAGC  
TTTGTTTGGGGAGATGTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA  
TTATTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA  
AATTTAGGGTCTGAATAGGAAGTTAATTCTCAAGAGTAAGTGAAGAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT  
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA  
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTGAAATA  
AAAATATTATATAAAAAGTAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPKGDSGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTNSNMTLRDRDFPWTTLMSLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWEAFEILDKLLDGDLTSDPSYFQNVTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRO  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

**Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338,  
348-352, 353-357, 424-428

**Tyrosine kinase phosphorylation site.**

amino acids 423-432

**N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

**Serine carboxypeptidases, serine active site.**

amino acids 200-208

**Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTCCGGCTCGGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT  
TTTCCCTTCCTAACAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGTTCTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGAGCTCCTTG  
CCTCTCTGCGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGAGGGCTGCCTAACAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGAAAGACTGGGTTAGTCCTAACAGTGGCTAACAGGAGCAGAAA  
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACAGGAGCAGAAA  
TAGAGATGCTTGAAATTTAAAAAGCAAGTATTTATAGCATAAAAGGCTAGA  
GACCAAAATAGATAACAGGATCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACACCAGGATGGGACCTGGTC  
AGGCCAGCCTTTGCTCCTCCCGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG  
ACAGCCGCTCTGTTGCTCTCAGTGGTCTGGGTGCTGGCCCCCCCAGCAGCCGC  
ATGCCTCAGTTCAGCACCTTCACTCTGAGAACATGTGACTGGACCTCAACCACGTGACCGT  
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAACAGGACAACAAGTCTGTTACCCG  
CCCCTCATCGTGAGCCCTGAGCGAAGTGTCTCACCTCACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCTGTGGAGCCTCTACCAAGGGTCTGCA  
AGCTGCTCGGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCAGTGTCAACAAGACGGGACCATGTAACGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTCATGGCACGGCTGTGGATGGAAAGCAGGATTACTTCCCACCCCTGTCCA  
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCATCAAGATCCCTTCAGACACCCCTGGCCTGGTCTCCACTTGACAT  
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGCTACTTCTACTGTCCAGCCGAGA  
CCCCTGAGGCTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTCCGG  
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCTGCCCTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCTGCAGGCTGTTACCTGGCCAAGCCTGGGACTCACTGGCCC  
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCTCCAAAGGGAGAAC  
CACTATCACCAACCGCCGATGACTCTGCCCTGTGCTTCCCTATCCGGGCATCAACTT  
GCAGATCAAGGAGCGCTGCAGTCTGCTACAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTTG  
TGGGGACTAAGAGTGGCAAGCTAAAAAGTAAGAGTCTATGAGTTAGCTATTGGTGGAGATTA  
ATTACCTCCTCAGCAAAGAGTCCCTCTGGAGGTAGCTATTGGTGGAGATTA  
GCAACTTATTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGGTTAATTG  
ACTTAGCTCTAGCTACTCCCTCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA  
TTCAATATTCCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAA

## **FIGURE 62**

MGTLGQASLFAPPGNYWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLLSVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTQHGTVGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTNTNNVNKLLIIDYSENRLLAGSL  
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL  
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFIAIFSKGQKQYHHPPDDSALCAFPRAINLQIKERLQSCYQGEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTSGKLKKVRVYEFRCNSAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

**Signal sequence:**

amino acids 1-32

**Transmembrane domain:**

amino acids 71-87

**N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

**Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328,  
383-387, 384-388, 471-475, 481-485, 530-534

**N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGC GGACTGGAGTGGGAACCCGGG TCCC CGCTAGAGAACACCGCGATGACC  
ACGTGGAGCCTCCGGGAGGGCGGGCCACGCTGGGACTCCTGCTGCTGGCTTGGGCTTGGTGC  
CCGAGGCTGGACTGGAGCACCCCTGGCTCTGGGCTCCGACAGCTGGGCTGCAGGCCAAGGGCT  
GGAACCTCATGCTGGAGGATTCACCTCTGGATCTCGGGGCTCCATCCACTATTCCTGTCAGGCCAAGGGCT  
TACTGGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTTGAACACCCCTACCCACCTATGTCCTGGAACCT  
GCATGAGCCAGAAAGAGGCAAATTGACTCTGGAACCTGGACCTGGAGGCCCTGCTCTGATGGCCGAG  
AGATCGGCTGTGGTGAATTCTCGTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGC  
TGGCTACTCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATT  
TGACCACCTGATGTCAGGGTGTGCCACTCCAGTACAAGCGTGGGGACCTATCTGCCGTGCAGGGAGA  
ATGAATATGGTCCCTATAATAAAGACCCCGCATACTGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATT  
GTGGAACTGCTCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGATTGTCCAGGGAGTCTGGC  
CAACTTGCAGTCACACACGAGCTGCAGCTACTGACCACCTTCTTCAACGTCCAGGGACTCAGCCAAGA  
TGGTGTGGAGTACTGGACGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTGGATTCTCTGAGGTT  
TTGAAAACCGTGTCTGCCATTGTGGACGCCGGCTCTCCATCAACCTCTACATGTCACGGAGGACCAACTT  
TGGCTTCACTGAATGGAGCCATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTG  
TGACAGAAGCGGGCATTACACGCCAAGTACATGAAGCTCGAGACTTCTCGGCTCATCTCAGGCATCCCT  
CTCCCTCCCCACCTGACCTTCTCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTGTACCTGTCTGTG  
GGACGCCCTCAAGTACCTGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGAGAACCTGCCAGTCATG  
GGGGAAATGGACAGTCTCGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGC  
GTGCATGATGGGGCAGGTGTTGTGAACACAGTACATAGGATTCTGGACTACAAGAACGAAGATTG  
TGTCCCCCTGATCCAGGGTACACCGTGTGAGGATCTGGTGGAGAACGTCAGTGGGGAGTCAACTATGGGAGA  
ATATTGATGACCGAGCGAAAGGCTTAATTGAAATCTCATGAAATGATTCAACCCCTGAAAACCTCAGAAC  
TATAGCCTGGATATGAAAGAGCTCTCTCAGAGGTTGGCTGGACAAATGGNTTCCCTCCAGAACAC  
CACATTACCTGCTTCTCTGGTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGG  
GCTGGGAGAAGGGGTTGATTGATCATCAATGCCAGAACCTGGACGTTACTGGAACATTGGACCCCCAGAAC  
CTTACCTCCCAGGCTGGTGGAGCAGCGGAATCAACCAAGGTACATCGTTTGAGGAGACGATGGCGGGCC  
TGCATTACAGTTCACGGAAACCCCCCACCTGGCAGGAACCAAGTACATTAAGTGAGCGGTGGCACCCCTCTG  
CTGGTGCAGTGGAGACTGCCCTCTGACCTGAAGCTGGTGTGCTGCCCAACCCACTGCAA  
AGCATCTCTTAAGTAGCAACCTCAGGGACTGGGGCTACAGTCTGCCCTGTCTCAGCTAAAACCTAAGCC  
TGCAGGGAAAGGTGGATGGCTCTGGCTGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCG  
AGGCTGTCGGCTGTCTAGGGTGGAGCAGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAGTGTG  
AAACGTGCCCTTGACCGGACGTACAGCCCTGCCAGCATCTGCTGGACTCAGGCGTGTCTTGCTGGTCT  
GGGAGGCTGGCCACATCCCTCATGGCCCATTATCCCCAAATCTGGGTGTGTCACCAGTGTAGAGGGTG  
GGGAAGGGGTGTCTACCTGAGCTGACTTGTCTCCTTCACAACCTCTGAGCCTTGGGATTCTGAA  
GGAACCTGGCGTGAGAAACATGTGACTTCCCCTTCCACTCGTGTGCTCCACAGGGTGACAGGCTGG  
GCTGGAGAAACAGAAATCCTCACCCCTGCGTCTCCAAGTTAGCAGGTGTCTCTGGTCAAGTGGAGGACA  
TGTGAGTCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGACAGAACGCCAGCTCACATGTG  
AGTCCTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTC  
CTGGCAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTC  
CAGAACGCCATGGCCATGTCTGCACATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTC  
CCCCCACGCCGAACAGCAGGGCAGAGCACGCCCTCTGAAGTGTGTCAGTGGCCCCGCTCCCCAC  
GGGGGCCAGCCAAACACCTGGCTTGGGCTCACTGTCCTGAGTTGCAGTAAAGCTATAACCTTGAATACAA

## **FIGURE 64**

MTTWSLRRR PART LGLLL VVLGFLV LRR LDWST LVPL RL RQL GLQAK GWN FMLED ST FW  
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEM DLGGLPSWLLQDPMRRLRTTYKGFTEAVDLYFDHLM SRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDNKGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKMVM EYWTGWFDSWGGPHNILD SSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSF GYI LY  
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLP EPTPLPAFFLG SLSIS  
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTL YLPGPWLS SGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

**Signal sequence:**

amino acids 1-27

**Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544,  
560-564

**N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293,  
309-315, 320-326, 366-372, 423-429, 425-431, 441-447, 503-509,  
580-586

## FIGURE 65

GGGGACCGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGTGGACGGGCCCCAGGACC  
CTGGTGAGGGTTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGCTCGGCCCGAGGCCCGAGGACCTCCATCTCCCAATGTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCTGCCTCGTCCCTGCTGCTGCCGTAGCCTGACGCTACTGCTGCCCA  
GGCAGACACTCGGTGTTGTAAGGGTCATGACCGGTTCTCTAGACGGGCC  
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGTCTGGGCCAC  
CGGCTTTGAAGATGCGATGGAGCGGCCTAACGCCATACAGTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA  
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG  
TGGGAGATGGGGGTCTCCATCCTGGTTGCTCGAAAACCTGAAATTCAAGAACCTC  
AGATCCAGACTTCCTGCGCAGTGGACTCTGGTTCAAGGTCTGCTGCCCAAGATATATC  
CATGGCTTATCACAATGGGGCAACATCATTAGCATTCAAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCGTCTT  
CGGAAGTATGAACCCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGCCAGAACATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC  
TCAAGTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG  
AATGGTCCGATAAGAAGGGACGCTTCCTCCGATTACTACCACTGACTATGATGCACC  
TATATCTGAAGCAGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTCCCTTGGGACCTTACCTCCCCCGAGCCCCAAGATGATGCTGGACCTGTG  
ACTCTGCACCTGGTGGCATTACTGGCTTCCTAGACTTGCTTGGCCCCGTGGGCCAT  
TCATTCAATCTTGCCTGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC  
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG  
AGACAAACTATTGGACGGGAAACTGGGTCCAAACTGGATATCTGGTGGAGAACATGG  
GGAGGCTCAGCTTGGGCTAACACAGCAGTGAACCTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTCCCTCCAGTTGCCAAAATGGCATATCCTCAAGCTCCTCTGGCCCCACATTCT  
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACCTGGGCCGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTACGTGCCAGATTCCCTGCTGTTCCTAGGGGAGCCCTAACAAAATTA  
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAGGTAGGCCGGCATGGTGGCTCATGC  
CTGTAATCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTAAACCCCCGTCTCCACTAAAATACAAAATTAGCCGGCGTG  
ATGGTGGCACCTCTAACATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC  
AGGAGGAGGAGGTTGCAGTGAGTGGAGGTTGACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFLYRTYMTHTIFEPTFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

**Signal sequence:**

amino acids 1-27

**N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

**Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473,  
550-554, 603-607, 644-648

**Tyrosine kinase phosphorylation site.**

amino acids 191-198

**N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229,  
227-233, 231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTGC  
ACCCACAATATGGCTTACATGTTAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT  
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT  
GCGTTCCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT  
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG  
AAAAACTCAGGCAGCACATTCAACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGTGGCCGATGCTGTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAAATTCTGCTAAGATTCTCAAATGACTAACCTCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA  
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCTGGGTGTATTGCTAAAAA  
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCAATTACAGGAACCTGGAT  
TTAAAGTCCAATAACATTGCAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT  
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA  
AAAACTGGAGTCACTTATTCTCTAACAAACAAGCTGAATCCTTACAGTGGCAGTATT  
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTCAATGATTCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG  
TGGAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTGCAAATGGGATTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG  
ATACATCTTTAAAATAACAGAGAGGATGCATAGAACGGCTGATAGAACACATAACTGAAT  
GTTCAATGTTGAGGTTTAAGTCATTCAAATCATTGTTTTAAATTGTTGTAACCTGGAT  
AAAGGGAAAGGAAAATTATAACTAACATCTGGTTCTTTAAATTGTTGTAACCTGGAT  
GCTGCCGCTACTGAATGTTACAAATTGCTGCCTGCTAAAGTAAATGATTAATTGACATT  
TTCTTACTAAAAAAAAAAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL  
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLLESLRELRHLKILHVKSNLTKVPSN  
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPIHAIFSLSNLQELDLKS  
NNIRTIEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ  
KLRCLDVSYNNISMPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

**Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

**Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

**N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCACGCGTCCGGCCTCTCTGGACTTGCATTCCATTCTTCACTGACAAACTGACTTTTTATTC  
TTTTTTCCATCTCTGGCCAGCTTGGGATCCTAGGCCCTGGAAAGACATTGTGTTACACACATAAGG  
ATCTGTGTTGGGTTCTTCTCCTCCCTGACATTGGCATTGCTTAGTGGTGTGGGAGGGAGACCACG  
TGGGCTCAGTGTGCTTGACTTATGCTTAGGTACATCGAAGTCTTGACCTCCATACAGTATTATGCC  
TGTGATCGCTGGTGGTATCTGGCGCTTGCTGATAGTTGTCGTGCTGTCTTACTTCAAATAC  
ACAACGCGCTAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAATCACAAACCCAGACAAGGTGTGG  
GCCAAGAACAGCCAGGCCAAACATTGCCACGGAGTCTTGTCTGCCCTGAGTGTGAAGGATATAGAAT  
GTGTGCCAGTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCCTTGAGTTAGGAAAGGCTCCC  
TTCTCAAAGCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTCAGGCACAGAAGA  
AAGGCACAGCTCCCATCAGTTCATGGAAAATAACTCAGTGCCTGCTGGAACAGCTGCTGGAGATCCCTAC  
AGAGAGCTTCACTGGGGCAACCTTCAGGAAGGAGTTGGGAGAGAGAACCTCACTGTGGGAATGCTGA  
TAAACCAGTCACACAGCTGCTTATTCTCACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGA  
GGTGTCCAGAAAGCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGCGCTTGCAA  
AATGGAGCTTGTGAGAAGGCTATGCCATTGACCCCTTAATTCTCTCTGTTGGGGAGCTGACAATGGCG  
AGGCTGAAGGCAATGCAAGCTGACAGTCAGTCTAGGGGTGCCAATATGGCAGAGAACCAAAGCCATGATC  
CTGCAACTCAATCCAGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAGCATCAGAATTATCTT  
TTCCTATGTCAGCTTGTGATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTGACGAACTCCAGCA  
ATGGGCCTCTGCTAGGGCAAGTCTGCAAGTAAAAGCAACTATGTTCTGTATTGAAATCATCATCCAGTACATTG  
ACGTTTCAAATAGTTACTGACTCAGCAAGAATTCAAAGAACTGTCTTGTCTTACTACTTCTCTCTCAA  
CATCTCTATTCCAAACTGTGGCGTTACTGGATACTTGGAAAGGATCCTCACAGCCCCATTACCCAAAGC  
CGCATTCTGAGCTGGCTTATTGTGTGGCACATAACAAGTGGAGAAAGATTACAAGATAAAACTAAACTC  
GAGATTTCTAGAAAATAGACAAAAGCTGCAAATTGATTTCTGCCATCTATGATGGCCCTCCACCAACTC  
TGGCCTGATTGGACAAGTCTGTCGGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTGACTGTGT  
TGTCTACAGATTATGCCAATTCTACCGGGATTTCCTGCTTCTACACCTCAATTATGAGAAAACATCAAC  
ACTACATCTTAACCTGCTCTGACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTAACTC  
TAATGGGATAACTGCAACTAAAGACCCAACTTGCAGACCCAAATTATCAAATGTTGGAATTTCCTG  
CTCTTAATGGATGGTACAATCAGAAAGGTAGAAGAGTCAGTCATTACTACCCAATATAACCTTCT  
GCATCCTCAACTCTGAGTGATCACCGTCAGAAACAACCTCAGATTATTGTGAAGTGTGAATGGACATAA  
TTCTACAGTGGAGATAATACATAACAGAAGATGATGTAATACAAAGTCAAATGCACGGCAAATAAC  
CCAGCATGGCTTTTGAAATCCAATTCTGAAAAGACTATACTTGAATCACCATAATTATGTTGGAAC  
CAAACCTTTTGTCAAGTTAGTCTGACACCTCAGATCCAAATTGGTGTGTTCTGATACCTGTAGAGC  
CTCTCCACCTCTGACTTTGCATCTCCAAACCTACGACCTAATCAAGAGTGGATGTAGTCAGAGTGAAC  
AGGTGTATCCCTTATTGGACACTATGGGAGATTCCAGTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTC  
GTGTATCTGCAGTGAAAGTTGATATGATAGCAGTGACCACAGCTCGCTGCAATCAAGGTTGTGTC  
CAGAAGCAAACGAGACATTCTCATATAAAATGGAAAACAGATTCCATCATAGGACCCATTGCTGTGAAAAGGG  
ATCGAAGTGCAAGTGGCAATTCAAGGATTTCAGCATGAAACACATGCGGAAGAACTCCAAACCAGCCTTCAAC  
AGTGTGCATCTGTTCTCATGGTTCTAGCTCTGAATGTGGTACTGTAGCGACAATCACAGTGAGGCAATT  
TGTAATCAACGGGAGACTACAAATACAGAAGCTGCAAGACTATTAACTAACAGGTCCAACCTAAGTGAGA  
CATGTTCTCCAGGATGCCAAGGAAATGCTACACATATTATGAATAAATGAGGAAGGGCCTG  
AAAGTGACACACAGGCCATGTAAAAAAA

## **FIGURE 70**

MELVRRLMPLTLLIISCLAELETMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVGRVTPTFESSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTSLTCCSDRMVIIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWTDSIIGPIRLKRDERSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

**Signal sequence:**

amino acids 1-24

**Transmembrane domain:**

amino acids 571-586

**N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

**Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375,  
379-383, 408-412, 463-467, 520-524, 556-560

**Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

**N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 71**

GACGGAAGAACAGCGCTCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATCGGCCCGAGGAGCTCCCAGGCTCGCGTCCCGTTGCTGCTGTTGCTGCTGC  
TGCTGCCGCCGCCGTGCCCTGCCACAGGCCACGCCGCTCGACCCCACCTGGAGTCC  
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG  
GGGAGTGTGTTCCGTGCCAGCTCGGTAGCGAGTGGTTCTGGTGGTATTGGAAAAGGAAA  
AGATAACCGAAGTATGTGAAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT  
TTTGGACCACTATTACAGCAAAATTGTTAATGCCAACAGTGGGAGATATTTCAGGC  
CTCTGGTGCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGGT  
CAGAATATTGTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCCTTGGACTGTACTATTCCCTTTGAA  
ATGGTTTCATCCGCTCTCCTGAGGATGAATCCAGTTCACTCCATAAGCGGCAATTCCAG  
TTTCTAACAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGTT  
ATATAATGAAAGCCCAGTCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTCTATACCTGCAGTGCAGTTATAACCCAGGACATCTTGCCA  
CATAAATGGGAAAATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG  
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGAG  
GAGCGACTGAGGCAAGTGGGTCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTCCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT  
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCATGGACAGCCACTTAAC TG  
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC  
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTTCAGCCCTTCCCTTTCCACTA  
AATTTTCTTAAATTACCATGTAACCATTAACTCTCCAGTGCACCTTGCATTAAAGTC  
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACGTGAAAATTATGTTGAAGCCATATCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT  
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCAGTACCAACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAAGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA  
GTTTTCTTCTCAATTATAAATTAACATAAGTGTACTGTAACCTACAAACGTTTAATT  
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIQFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIQPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

**Signal sequence:**

amino acids 1-28

**N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

**Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280,  
315-319, 375-375

**Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

**N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

**Leucine zipper pattern.**

amino acids 410-432

**Alpha-L-fucosidase putative active site.**

amino acids 283-295

## **FIGURE 73**

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCAAGGCTTTGCGTGAGAAGAGCT  
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAGGGGAACCAGC  
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGCAAG  
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACCTGCAGCTATGGCTGGGTTGGAGA  
TGGATTCTGGTCATCTAGGATTAGCCAACCCCAAGTGTGGAAAAATGGGTTGGGTG  
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATGAT  
ACTTGGACTAACCGTGCATTCCAGAAATTATCACCAACAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCACTTCTATTCCACGG  
AGAAAAAAATTGATTGTGTACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC  
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAAGCTGGTCTTGGATTTC  
TATGTCAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCATGATAGCAACCTTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGAAACTACCGTGCATGCCGGAA  
CCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC  
TTACCCCTGCCCAAGCTGGGAAATCAAAAGGCCAAGAACCAAAGAACAGAAAGTCCACCCCTT  
GGTTCTTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAATGC  
CCTTCTCCTTATTGTAACCCCTGCTGGATCCTATCCTCCTACCTCCAAAGCTCCACGGCC  
TTTCTAGCCTGGCTATGCTCTAATAATATCCCACGGAGAAAGGAGTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGTTAAAAGGCCCTGGCTGTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC  
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTCTGAGCCGGTA  
AGAGCAAAGAAATGGCAGAAAAGTTAGCCCCTGAAAGGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA  
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCTCT  
AGGAAATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA  
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTCTCA  
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTCTATTCTGAGACTAATCTT  
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTATAACATACCTAAGAAG  
TACATTGTTACCTCTATATAACCAAGCACATTAAAAGGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA  
AGCATTAGAAAACCTT

## FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF  
AAVCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASFNEAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP  
SKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 75**

AGAGGCGGTCTGGCACCTCTAATTGCTCTCGTGTATTGGTGCAGCGACTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTTACTCGTGAGGAA  
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT  
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCACTGGATTGTGGAGTTCTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC  
GTACAGGGCTAAATTGGAGGTGGATGTTGGACGCTATACTGATGTTAGTACCGGTAC  
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGTATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTTCTG  
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCAAGTGTCAA  
TGGGAAAACAAGAAGGATAAAAGATCCTCACTTGGCAGTGCTCCTCTGTCAATT  
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG  
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGAATTGTCAG  
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGAAATGGTTCCCTCAAGCTTGGTCAGTGTGTTACTGCTTATC  
AGCTATTGACACATCTCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG  
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA  
CGCTAAGAATTTCACCCCAAGGACTCTGCTCCTTAAGCCCTCTGGCTTCGTTATGGTC  
TTCATTAAAAGTATAAGCCTAACCTTGTGCGTAGTCCTAAGGAGAACCTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTCAC  
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT  
TCCTTTG

## FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAFLVRKLPPCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

**Signal sequence:**

amino acids 1-48

**Transmembrane domain:**

amino acids 111-125

**N-glycosylation site.**

amino acids 165-169, 185-189

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

**Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

**N-myristoylation site.**

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## **FIGURE 77**

GGACAGCTCGCGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG  
GGGCCCCAGCCTGGCCGGGTACCCCTGGCATGAGGAGAGGGGCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTACGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGTACGAGCCGGCCCTGGTCTCCCCGGCGGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCCGTGCACCTGCCGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCCGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGGCTGG  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGCTTTCTTACCAAGTCCCCCA  
ACGGGCCTACCAAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAAGCAGGCTGCCGTG  
GTGGCCTCTTGAGCAGCTCTCCGGGCTGGAGGGAGGGCTGGACTGGTGCAACGCCGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCATCATGTTGCCCGGAGCCCTGCCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCGTAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC  
AGCTCTTGCCGCCTGGAAGTTCCATGGCCTGGACCGCTGCCAGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCTGTGGTCACCCGATCCTAACTGTGGCCCCCAGAGCCTGGG  
CCGAAGCTTGGCTCCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCCCTGCCGATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT  
CGTTTCCCTGTGGTTGGAGCCATTAACTGTTTTACTTCTCAATTAAATTCT  
TTAAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG  
GATGCCCACTCCAGGAATCATGCTTGCCTCCCTGGGCATTGCGGTTTGTGGCTTCTG  
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCTGGCAGAGTGGG  
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGGATGGTGGGCACAGTTCTCCCTGCC  
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCTCCGGAGCTGGCTTGGCCTCTGCC  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTCCAGGCAGGAAATCTGAGGGAAAGAAACTCCCTCCCCGTTCCCT  
TCCCTCTCGGTTCAAAGAATCTGTTGTGATTGTTCTCCTGTTCCCTGTGTGG  
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGTATGACTGCCCTCCGCCAA  
AA  
AA  
A

## FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

**Signal sequence:**

amino acids 1-17

**Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

**Tyrosine kinase phosphorylation site.**

amino acids 137-145

**N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## **FIGURE 79**

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GATGAT**GTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTATGGC  
CAGGGGAGGGTGCACCAGGCAGGCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA  
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA  
CCCCAGAGGAAGCCAGGCCGTCTGGGGCGATCGTGGACCGCATGGACCGCGCGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGGA  
CATACGGACTCGGTGAGCGCGGCCCTGGACACGTACGACACGGACCGCAGGGCGTGTGG  
GTTGGGAGGAGCTGCGAACGCCACCTATGCCACTACGCGCCGGTGAAGAATTGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGACGAGCGCGTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGACATCGTGAATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCA**GGTGGAGGAGTACATCGCGATCTGTACTCAGCCGAGCCTGGGAGGA**  
GGAGCCGGCGTGGGTGCAGACGGAGAGCAGCAGTCCGGACTTCCGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGACCC  
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA  
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCT**GAGCTGTGAGCACCAGCAGCAGCCTGCCACAGCCTCAGAGGCCG**  
CACAATGACGGAGGAGGGGGCGTGTGGCTGGCCCTCCCTGTCCAGGCCCCGAGGAG  
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC  
TGTCCCTGTCACACCCCAACCCAGGGAGGGCTGTCAAGTCCAGAGGATAAGCAATAC  
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCT  
GGCCCCAGCCCTCTCCTGCCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA  
AAGCCAGCGCCGGACCTTGAAAAA  
AAAAAAAAAAAAAA

## FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPEEFPHMRDIVAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ  
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

**Signal sequence:**

amino acids 1-20

**N-glycosylation site.**

amino acids 140-144

**Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

**N-myristoylation site.**

amino acids 263-269, 311-317

**Endoplasmic reticulum targeting sequence.**

amino acids 325-330

## FIGURE 81

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCTGTTCTTGTGCTCCAG  
CCTGTCGTCGTCGTTGGCGCCCCGCCTCCCCCGGTGCGGGGTTGCACACCGATCCTG  
GGCTTCGCTCGATTGCCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTGTCCTCTCCTCTGCCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT  
GAGGAGGTGACGCCGCCCTCCGCACCCCTGGCCTGCCGATCTCCCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGCCCGCAGCAGGGAGCCGCTCCATTGCTATCACATG  
TTTACACAGAGGCTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGCTGCC  
CTCTTGAGGAATTCTCTGTATGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACCGAGTCTATAGCCTACC  
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTCACAGTAACAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACACCCGAGAAGAAAACGG  
CAATAAAGATTGAAAGCAGACATTGCATTGATGGAAGCTTAATATTGGCAGC  
GCCGATTAAATTACAGAAGAATTGTTGGAAAAGTGGCTTAATGTTGGGAAATTGAACA  
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA  
AAACTTACATCAGCAAAGATGTTTGTGCAATAGGAAAGTAGGTTTAGAGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTTGGCCTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAAGGATGTACATTTGTTGACAAGGCTGTCTG  
CGGAATAATGGCTTCTCTTACACATGCCAACACTGGTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGCACTCATGAACAAATGATGTGCAAGACCTGTTAACT  
CAGTGAACATTGCCTTCTAATTGATGGCTCAGCAGTGGAGATAGCAATTCCGCCTC  
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAGAAGAT  
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT  
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCCCTATAAGGGAGAGGCCAACAGAA  
CTTCCTAGTAATTGTCACAGATGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAAGGAACTCACTATCTCTGTTGGTGGCTGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGGAGTCTCACGCTTCTTCACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAACATTGACAACTGAAAGAAAAGTACAAGGGATCCAGTGTAAATTGTATT  
CTCATAACTGAAATGCTTCTGATGTCATCAGAACAGCTACTAAGTAAACTTAAAGTATGTCAAC  
AGCCATTAGGCAAATAAGCACTCCCTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT  
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTCTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAACCTTAAGAGTTCAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAGAATCTGATACCTAGACCAAAAAAA

## FIGURE 82

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDLFAIKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

**Signal sequence:**

amino acids 1-24

**N-glycosylation site.**

amino acids 100-104, 221-225

**Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381,  
420-424, 425-429, 478-482, 528-532

**N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

**Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGACCCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC  
GGCGGCCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGAACTCGGTCCAGTCG  
GGCGCGGGCTCGGGCGCAGAGCGGAGATGCAGCGGCTGGGCCACCCCTGCTGTGCCTGC  
TGCTGGCGGCGGGTCCCCACGGCCCCCGCAGCGACCTCGGTCCAGTC  
AAGCCGGCCCAGCTCTCAGTACCCGAGGAGGGCACCCCTCAATGAGATGTTCCCGGA  
GGTTGAGGAAGTGTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGCTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGAGCAAGGGAGCCACCGAGTCATCATCGACGAGGACTGTGGGCCAGC  
ATGTACTGCCAGTTGCCAGCTTCAGTACACCTGCCAGCCATGCCGGGAGAGGATGCT  
CTGCACCCGGGACAGTGAATGCTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA  
TGGCCACCAGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG  
TGCTGTGCCTTCCAGAGAGGGCTGCTGTTCCCTGTGTCACACCCCTGCCGTGGAGGGCGA  
GCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG  
GAGCCTGGACCGATGCCCTGTGCCAGTGGCCTCCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCACCTTCGTGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT  
GCACTGCTGGAGGGAGAGATTAGATCTGGACCAAGGCTGGTAGATGTGCAATAGAA  
ATAGCTAATTATTCAGGTGTGCTTAGGCAGGGCTGACCAAGGCTTCTTCTACA  
TCTTCTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTGCAATTGTTCA  
TCCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAC  
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCTTGCCTTACCA  
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA  
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTCTTCCATGGCATAGGTAAGCTG  
TGCCTCAGCTGTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCA  
AGCAGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCA  
CCTCTCAGCACAGCCTGGGAGGGGTCTTGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTGCCAGTCACACAGCTAGTGAAGACCAGAGCAGTT  
CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTGGTGC  
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTGGTCTTGAGGCATGCACATCTGG  
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGT  
AGTGTGGGCAGCCGTCTCTAATGAAGACAATGATATTGACACTGTC  
TGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAAC  
GTACTTAGGTAATTGTAGGGAGGATTATAATGAAATTGCAAATCA  
TGAAGACAATTATCAACCAACGTGGAGAAAATCAAACCGAGCAGGGCTGTG  
GTAATATGCGACTGCGAACACTGAACACTACGCCACTCCACAAATGATGTT  
TGGACTGTTGCCACCATGTATTCCAGAGTTCTTAAAGTTAAC  
TAAGCATGCTTCTTGAGTTAAATTATGATAAAACATAAGTTGC  
ATAAATCACTCAACTGCAAAAAAAAAAAAAAAA

## FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRSAVEEMEAAEAAKASSEVNLPPSYHNETNTDTKGNNTIHVREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVHQELEDLERSLTEEMALGEAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCT  
GAAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCAAACACACATGTGCATGTACACACACACATA  
CACACACATACACCTCCTCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGA  
CACTAAAGCCTTAAGGACAGGCCTGGCATTACCTCTGCAGCTCCTTGCTTGTGAGTCAGGAAACATGGGA  
GGGGCCAGGCACGGTCACTCACACCTGTAATCCCAGCATTGGAGGACAGGAGGTGAGCAGATCACTTGAGGTC  
AGGAGTTGAGACCAAGCCTGGCCAACATGGAGAAACCCCCATCTACTAAGAAAATACAAAATTAGCAGGAGT  
GGTGGCAGGTGCTGTAATCCCAGCTACAGGTGGCTGAGCCAGGAGAATCGCTGAATCCAGGAGGCGGAGG  
ATGCAGTCAGCTGAGTCACCGCTGCACCTCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACA  
CGGGAGGAGGGTAGATACTGCTTCTCTGCAACCTCTTAACCTCTGCATCCTCTTCCAGGGCTGCCCTGA  
TGGGGCCTGGCAATGACTGAGCAGGCCAGGCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAA  
GTGACGCCCGGTGAGAATGACTGCCCTGGGAGGGTGGCTTCTGGGCCCTGGCAGGGTTGCTGACCCCTACCC  
TGCAAAACACAAAGACAGGACTCCAGACTCTCTTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCT  
TCTCGTGGCCCCACTCTTGTAGCTTGGTGGCTGGTGCCTGCCACTGCCACTGTGCCCTGGTACCCCTGGCATGTT  
CCTGCCCTCTAGTGTGCCAGATCCGGCCCTGGTATAACGCCCGCTCGCCTACCGCGAGGCTACCCACT  
GTGGACTGCAATGACCTATTCTGACGGCAGTCCCCCGGACTCCCCGCCAGGACACAGACCCCTGCTCTGCA  
GAGCAACAGCATTGTCGTGGACCAGAGTGAGCTGGCTACCTGGCAATCTCACAGAGCTGGACCTGTC  
AGAACAGCTTCGGATGCCAGACTGTGATTTCATGCCCTGGCCAGCTGCTGAGCCTGCACCTAGAGGAG  
AACAGCTGACCCGGCTGGAGGACACAGCTTGTGAGGCTGGCCAGCCTACAGGAACCTATCTCAACCAAC  
CCAGCTTACCGCATGCCCTGGCCAGGGCTTCTGGCCTCAGCAACTTGCTGCCCTGCACCTCAACTCCAAC  
TCCGTAGGGCCATTGACAGCCCTGGTTGAAATGCTGCCCAACTTGGAGATACTCATGATTGGGGCAACAAAG  
GTAGATGCCATCTGGACATGAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCT  
GGGGAGATCTCGACTATGCCCTGGAGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAAGCTGG  
CCCGGGTGCCTGGCCAGGGGGACTTGGCAACATGCTGCCCTTAAGGAGCTGGACTGAAACAACATGGAGGAGTGG  
CTCCATGACAAGTTGCCCTGGTGAACCTCCCCGAGCTGCCAGAAGCTGGACATCACCAATAACCCACGGCTGT  
CCTTCATCCACCCCCCGCCTTCCACCCACCTGCCAGATGGAGACCCCTCATGCTCAACAACAACGCTCTCAGT  
GCCCTGCAACAGCAGACGGTGGAGTCCCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCATCCGCTG  
TGACTGTGTCATCCGCTGGGCAATGCCACGGCACCCGTGTCGCTCATGAGCCGAATCCACCTGTGTG  
CGGAGCCTCCGGACCTCCAGGCCCTCCGGTCCGTGAGGTGCCCTTCCGGAGATGACGGACACTGTTGCC  
CTCATCTCCCACGAAGCTTCCCCCAAGCCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCATTGCCGGC  
ACTGGCCGAACCGAACCCGAGATCTACTGGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAAGCA  
GGAGGTACCGGGTGTACCCGGAGGGACCTGGAGCTGCCAGGGTGAACAGCAGAAGAGGCAAGGGCTATAACACC  
TGTGTGGCCCAGAACCTGGTGGGGCTGACACTAACAGGGTAGTGTGGTGTGGCCGTGCTCTCCTCAGCC  
AGGCAGGGACGAAGGACAGGGCTGGAGCTCCGGGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGG  
TCACCCCCACCAACACAGTGTCCACCAACCTCACCTGGTCCAGTGCCTCCTCCCTCCGGGAGGGCCACA  
GCTCTGGCCCGCCTGCCCTGGGAACCCACAGCTACAACATTACCCGCCCTTCAGGCCACGGAGTACTGGG  
CTGCCCTGCAAGTGGCTTGTGATGCCACACCCAGTGGCTTGTGATGGCCAGGACAAAGAGGCCACTT  
CTTGGCCACAGAGCCTTGGGATGTCCTGGCTATTGCCACCTGGCTCCTGGCTGCTGCTCTTCTCTGGCAGCT  
GGCTAGGGCCACCTGGCACAGGCCAACCCAGGAAGGGTGTGGTGGAGGCGGCCCTCCCTCCAGCCTG  
GGCTTCTGGGGCTGGAGTGCCCTTCTGTCCTGGCTGTGCTCCCTCGTCTGCCCTGGAATCCAGGGA  
GGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCCACCATGTCCTCAAATTTCTGAGCTCAGCCTGT  
TCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAAAGAGAACAGTCTGGGCCAGATGCCCTGCCAGG  
AAAGGGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGGCCAAGACAGATGGGCTTGTGGCCCTGGGGT  
GCTTCTGAGCCTGAAAAAGTTGCCCTACCTCTAGGGTCACTCTGCTGCCATTCTGAGGAACATCTCCAA  
GGAACAGGAGGGACCTTGGCTAGAGCCTCTGCCCTCCCCATCTCTCTGCTGCCAGGGCTCTGGGCCCTGG  
TGGCTGTCCTTACCTGTGTCCTGGGCTGCACCCCTTCTCTTCTGTCAGTCTCAGTTGCT  
TCTTGTGCCCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCACCTCGGGGGCTGCCCTCAATGTGGAGT  
GACCCCAAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAACGCCCTCATCTCAGCAGCCTGGGCC  
CATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAAATGTGTACACCTCCCCAACCGATT  
ACTCTTTCTCCTGTTGAAAAATAAAATAACAATAACAAAAAA

## **FIGURE 86**

MRLLVAPLLLAWVAGATATPVVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDSQNSFSDARCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLAGMNLREISDYALEGLQSLFSDYDNQ  
LARVPRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP  
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAAGRRYRVYPEGTLELRRVTAAEAGLYT  
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLAAGLA AHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV  
SAPLVLWPWNPGRKLPSSSEGETLLPPLSQNS

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 629-648

**N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

**Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

**Tyrosine kinase phosphorylation site.**

amino acids 532-540

**N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

**Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCC  
TCTACATCGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCAC  
AACATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCTGACGGCTACCGCACCTACCGCTGTGCCA  
CCCCCTGGCCACACTCTCAAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTCTACGGCTCATCTGCA  
TGTACACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGC  
TACAGCGACATCCCCGACGTCAAGAACGACTTCGCCCTCATGCTGCACCTCATTGACCAATACGACCCGCTCA  
CTCCAAGCGCTTCGCCCTTCCCTGCGAGGTGAGTGAGAACAGCTGCGGAGCTGAACCTCAACAACGAGT  
GGACGCTGGACAAGCTCCGGCAGCGGCTACCAAGAACCGCAGGACAAGCTGGAGCTGCACCTGTTATGCTC  
AGTGGCATCCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCCTCAAGCTGGAGCTGATCCCCGACGTGAC  
CATCCCAGCATTGCCCAAGCTCACGGGCTCAAGGAGCTGTTGAGCTACCCACACAGCGGCAAGATTGAAG  
CGCCTGCCCTGGCCTTCCCTGCCGAGAACCTGCGGGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCG  
CTGTGGATCTATAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGCGAGAACAAACGCTA  
CATCGTCATCGACGGGCTGCCAGCTCAAACGCCCAAGGTGCTGCCGCTCAAGAGAACCTAAGCAAGCTGC  
CACAGGTGGTCACAGATGTGGCGTGCACCTGCAGAAGCTGTCATCAACAATGAGGGCACCAAGCTCATGTC  
CTCAACAGCCTCAAGAACGATGGCGAACCTGACTGAGGCTGATCCGCTGCACCTGGAGCGATCCCCA  
CTCCATCTCAGCCTCCACAAACCTGCAGGAGATTGACCTCAAGGACAACAAACCTCAAGAACCATCGAGGAGATCA  
TCAGCTTCAGCACCTGCACCCCTCACCTGCCCTAAAGCTGTTGACAACACATGCCCTACATCCCCATCCAG  
ATCGGCAACCTCACCAACCTGGAGCGCCTTACCTGAAACCGCAACAAGATCGAGAACAGATCCCCACCCAGCTTT  
CTACTGCCCAAGCTGCCTACCTGCCACCTCAGCCACAACAAACCTGACCTTCCCTCCCTGCCGACATGCCCTCC  
TGCAGAACCTCCAGAACCTAGGACATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCG  
AAGCTGCCGCCCTGCACCTGGCAACACGTGCTGCAGTCACCTGCCCTCCAGGGTGGCGAGCTGACCAACCT  
GACGCAGATCGAGCTGCCGGCAACCGGCTGGAGTGCCTGCTGGAGCTGGCGAGTGCCACTGCTCAAGC  
GCAGCGCTTGGTGGAGGAGGACCTGTCACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCT  
GACAAGGAGCAGGCCTAGCGAGGCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCCCAGGCCGG  
AGGGCAGGCCTAGCTTCCAGAACCTCCGGACAGCCAGGACAGCCTGCGGCTGGCAGGAGCTGGGCC  
GCTTGTGAGTCAGGCCAGAGCGAGAGGACAGTATCTGTTGGCTGGCCCTTCTCCCTGAGACTCACGTC  
CCCCAGGGCAAGTCTGTGGAGGAGAGCAAGTCTCAAGAGCGCAGTATTGATAATCAGGGCTCCCTG  
GAGGCCAGCTCTGCCCAAGGGCTGAGCTGCCACCAAGAGGTCTGGACCCCTCACTTAGTTCTGGTATT  
TTTCTCCATCTCCACCTCCATCCAGATAACTTACATTACATTCCAAAGAAAGTTCAGCCAGATGGAAGGTG  
TTCAGGGAAAGGTGGCTGCCCTTCCCTGTCCTTATTAGCGATGCCGCCGGCATTAAACACCCACCTGG  
ACTTCAGCAGAGTGGTCCGGCGAACCAGCCATGGACGGTCACCCAGCAGTGCCTGGCTCTGCCGTG  
CGGTCCACGGAGAGCAGGCCTAGCTGGAAAGGCAGGCCTGGAGCTGCCCTTCAGTTTGAGCTT  
TTAGTTTTGTTTTTTTTAATCAAAAAACAATTTTAAAAAAAGCTTGAAGGATGGATGGTT  
GGGTATTAAAAAGAAAAAAACTTAAAAAAAGACACTAACGCCAGTGAGTTGGAGTCTCAGGCCAGG  
GTGGCAGTTCCCTGAGCAAAGCAGCCAGACGTTGAACTGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTG  
TCTTCCGGATCTGGTGTGACCTGGTCAGGAGTTCTATTGTTCCCTGGGAGGGAGGTTTTTGTTGTT  
TTGGGTTTTTTGGTGTCTTCTTCTTCTCATGTGCTTGGCAGGCACTATTCTGTGGCTGTGCC  
CAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGACTCGGGTTGGCTAATCCCGGATGAACGGTGCCTCCA  
TTCGACCCCTCCCTCTGCCCTGCCCTGCCCTCCACGCACAGTGTAAAGGAGCCAAGAGGAGGCCACTTCGC  
CCAGACTTGTGTTCCCACTCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCC  
CCCTGTCGCCACCTGGCTTCAAGAGCAGACACTTAGAGGCTGGCGGAAATGGGGAGGTGCCCTGG  
AGGGCAGGCCTGGTCCAAGCCGGTCCCGTCCCTGGCGCTGGAGTGCACACAGCCCAGTCGGCACCTGGT  
GCTGGAAAGCCAACCTGCTTGTAGATCACTGGTCCCGACCTTAGAAGGGTCCCGCTTAGATCAATCAGTGG  
ACACTAAGGCACGTTTAGAGTCTTGTCTTAATGATTATGTCATCCGCTGTCCGTCCATTGTGTTCT  
GCGTCGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAGCCTCTGACAACCATGAAGCAAAACCGTT  
ACATGTGGGCTGAACCTGTAGACTCGGTACAGTATCAAATAACAGAAAAAAACCGTT

## **FIGURE 88**

MRQTIIKVIKFILIIICYTVYYVHNIFKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRLQNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVFLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFRLRENLRALHIKFDTIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAYIPIQIGNLTNLERLYLNRNKIEKIPQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPP ELFQCRKLRALHGNVQLQSLPSRVGELETNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

**Transmembrane domain:**

amino acids 51-75 (type II)

**N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436,  
491-495

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

**Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTCTCCTGAAGACCTTCTCAGTTGCCACAAAG  
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTCAACTTGC  
GGGGGT TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTCA  
CGC CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCC  
CAGAAAGAA GCTCAAAATTATTCCCTGAGGATCAATCCTGGGAGGCCAGGCTACCA  
ACGTCTTGTGAACAAGTGGGAGGTGCTGGAGCTGGAGGCTGGAGGCAGGGATC  
AACGTGACGGTGATAATGGACAGCTGGATCTCATCGTAGATACCATGGGT  
CAGGAGGCCTG GGTGCGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCA  
AGTCTACAAGAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCAATGGTCTCTGACCAAGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAUTCAAGAAGATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGAGGAAGGCCATTCTCC  
CTGTATCT AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGG  
ATAAAATCATTGTCTCTGGAGGCAATTGGAAATTATTCTGCTTCTTAAAAAC  
CTAAGATTTTAAAAATTGAT TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFPSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLANVNKGLYRE  
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLWPELPKFSQLKWKALYSDPKSLETSASFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

**Signal sequence:**

amino acids 1-25

**N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

**Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355,  
449-453

**N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTAGTGATCCCTCCGGTGGATG  
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCAACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCCTGTCTCCAG  
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAAC  
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG  
GTCGGCCAATCGGCCCGGTGTCTACACCAATATGCCACCACTTGAGTGGATCCAGAAC  
CTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCCCTCTGGCCACTACTCTTTCCCTCT  
TCTCTGGCTCTCCACTCCTGGGCCGGTCTTGAGCCTACCTGAGCCCAGCAGCCTGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAACFETYSSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWSYIKEDEALP  
SPHTLQEVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

**Signal sequence:**

amino acids 1-18

**N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

**Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

**N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

**Amidation site.**

amino acids 33-37

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

**Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCTCTAGGGCT  
CTTGCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGTCCCTGGCGTGCGGACCCCTGAGGAAGAGCTGAGTCTCACCTT  
GCCCTGAGACAGCAGAATGTGAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCCTCCACACGGTCAAAAATGGCTCTTGCAGCCGGAGCCAGAAGTGCCATTCT  
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCC  
TGGGCTGAGTTCATCACTATGTGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTTGACTTTGTGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCCGTGAGCCGAGGTGACAGGGACTGTAGGCCCT  
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATACAACATTGACCTACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCCTGGTGCACATCTCACCTGGCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGGAGCCCTGCAGTGGCTATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGTCA  
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTTGCCTCAGGTGACAGT  
GGGGCCGGGGTGTGGTCTGTGAGACACCAAGTCCGCCACCTTCCCTGCCTCCAG  
CCCTATGTCACCACAGTGGAGGCACATCCCTCAGGAACCTTCATCACAAATGAA  
TTGTTGACTATCATGGTGGTGGCTTCAGCAATGTGTTCCACGCCCTCATACCAGGAG  
GAAGGCTGTAACGAAGTCCCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATTCCATGGGTCCGGAACCTGCCCTACTCCAGTGTGTTGGGGATCCTA  
TCCTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAAG  
GCTTACCAGCAGCATGGGCAGGTCTCTTGATGTAACCGTGGCTGCCATGAGCCTGTC  
TGGATGAAAGAGGTAGAGGGCAGGGTTCTGCTCTGGCCTGGCTGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCTTCTATC  
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTACTCCCTAACCCGTAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCACT  
CCTGCCTTAGATCCTCAATAAGATGCTGTAACTAGCATTGGATGCTCTCCCTCCGC  
ATCTCATCTTCTCTTCAATCAGGTTTCAAAGGGTTGTATAAGACTCTGTGACTA  
TTTCACCTGATATTCATCATCCCCAATTCACTGCAAGGAGACCTACTGTCACCGTTTACTCT  
TTCCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATCTCAATCTTGTTTATG  
GCCTTCCATCATAGTTGCCACTCCCTCCCTACTTAGCTCCAGGTCTTAACTTCTCTG  
ACTACTCTTGCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCAATTGC  
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTLMKAAARGLTLFASGDGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

**Signal sequence:**

amino acids 1-16

**N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

**Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

**Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

**N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## **FIGURE 95**

GGCGCGCGCTCTCTCCGGCGCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC  
GGGCTGCTCGGCGGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC  
TTCTTCTGCTCTGTGCTGTTGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTG  
GCCTGCATACCGCCTCCCTGCGTCTTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT  
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTATAAGGAACT  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC  
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC  
AGGTTCAGCATTGGGAAGGACTTCCTGCTCAACTACCCCTTCTAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCTGGTGGCAGAGAACATGTCTCACAGCTGCCACTGCA  
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCC  
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTCAGCCATGCCGAGCAGATGAA  
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACTTCTC  
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGTCTGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTCAGG  
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC  
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG  
TGACACAGTGTCCCTGGCAGCAATTAGGGTCTTATGTTCTTATTTAGGAGAGGCC  
AAATTGTTTTGTCTTGCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTAAAGGTGT  
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATCTG  
GTTTGTGTATCATATCATATCATTTAAGCAGTTGAAGGCATACTTTGCATAGAAATAA  
AAAAAAATACTGATTGGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG  
CAAACTTGATTTTATTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA  
CAAGAGATATGAAAAA

## **FIGURE 96**

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQSTLNLA  
KPDFGAEAKLEVS  
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTE  
TQVGIFYILSSSGDGAQHRDSGSSGK  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVA  
EKGVLTAACIHDGKTYVK  
TQKLRVGFLKPKFDGGRGANDSTS  
AMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYD  
A  
LLELKPKHCRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPG  
NLVYRFCDVKDETYD  
QQCD  
AQPGASGSGVYVRMWKRQQQKWERK  
IIGIFSGHQWDMNGSPQDFN  
AVRITPLKYAQICYW  
IKGNYLDCREG

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 93-97, 207-211

**Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

**Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

**N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320,  
338-344

**Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATGCCCTGGGTCTCTGAGCCTGCTGCCCTGCTCCCCGCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACC GGTTGTGGCGGCAGGACAGCACTGACAGCAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAAGCCGCTGGGTGATC  
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGAACCTGGCTCTCGTCCCAGAAGGTGGTGTGCCTGGTGGAGC  
CCCACCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGTCTGCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTG  
CCCACCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTGTCTGGCCACTCCGGGGCCCCCTATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGC  
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTGAAGGGGTGCA  
GCTCCGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG  
CCGCGCGCTCCTAGGGCCAGCGGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGGCGGCCCTCGGGCGTTTCCCCCGCTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCGGACGGCTGCTGGGAAGGAAACCCCTCCCCGACCGCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCAAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTTTAT  
AGGTATTTGTAACCTGCCACATATCTTATTTATTCTCCAATTCAATAATTATTATT  
CTCCAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318  
><subunit 1 of 1, 317 aa, 1 stop  
><MW: 33732, pI: 7.90, NX(S/T): 1  
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI  
PVPPACGKPQQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF  
SVLLGAWQLGNPGSRSQKVGVAV  
WVEPHPVYSWKEGACADIALVRLERSIQF  
SERVLPICLDPASIHLPPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVC  
SHLYWRGAGQGPITEDMLCAGYLEGERDA  
CLGDSGGPLMC  
QVDGAWLLAGII  
ISWGEGCAERNRPGVY  
ISLSAHR  
SWVEKIVQGVQLRGRAQ  
GGGALRAPSQG  
SGAAARS

**Signal sequence:**

amino acids 1-32

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459,  
528-534, 612-618, 623-629, 714-720, 873-879

## **FIGURE 99**

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGCCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCCAC  
AACAAAGGAGCGCGGGCGCCCGGGGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGGTGAAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAACGTGAGGCCCATCCTCCGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGTACTCCTTCCCTAGCAACGGGATTCCGGTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGGAAACCCAGGCC  
CCAACCTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC  
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGGCCAGTTA  
CCTTCCCCAAATGACCCATGTTCCATCCAAAATCAGCAGACAAAGTGACAGACAAACAA  
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG  
GGAACCTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCCTCAGTG  
AGGTCTTGGCCTCAGTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGCACACCTCCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTATGTGTGGGGCCCTCCTGGGA  
CTACTGCTCCTGCCTCTGGTGTGGATCTTCTTGAATGGGATACCAACTCAAAGGG  
TGAAGAGGTCACTGCTCCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA  
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC  
GGGCCACACCTCCTGCCCTCCCTGGTGTGGCTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG  
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC  
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFMLLLLPLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMVPLAMEEWHHEREHYNSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTEVPSILAALSPLSDEEPVTFPKS  
THVPIPKSADKVTDKVPSRSPENSMDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPPLLGLLLLPPPLVLAGIF

**Signal sequence:**

amino acids 1-22

**N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

**Glycosaminoglycan attachment site.**

amino acids 439-443

**Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

**N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186,  
231-237, 250-256

**Amidation site.**

amino acids 82-86, 172-176

**Peroxidases proximal heme-ligand signature.**

amino acids 287-298

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## **FIGURE 101**

GTAACCTGAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAATTGGTCATTCTCAAGTTATGGGGACG  
TACTTCTGTTCTCCCTCTGCTTGCACATTAGCAGACCGACTTAAGTCACAACAGATTATCTTC  
ATCAAGGCAAGTCCATGAGCACCTCAAAGCCTCGAGAACTGAACAAACATGAATTGGAGACCAT  
TCCAAATCTGGGACCACTCGGAAATATTACACTCTCTGGCTGGAAACAGGATTGTTGAAATACTCC  
CTGAACATCTGAAAGAGTTCACTGGACCTAGCAGCAACAATATTCAGAGCTCAAAC  
GCATTCCAGCCCTACAGCTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGGAACCTGGTATT  
TGACAATTGGCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGT  
TTAAACTGCCCAACTGCAACATCTGAATTGAAACCGAAACAAGATTAAAATGTAAGATGGACTGACATCCAA  
GGCCTTGGGCTCTGAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGG  
GCTGAGCAACATGAAATTTCAGCTGGACCATAACACCTAACAGAGATTACCAAAGGCTGGCTTACGGCT  
TGCTGATGCTGCAGGAACCTCATCTCAGCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTTCTGC  
CAGAAGCTCAGTGAGCTGGACCTAACCTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAAG  
CTTACTAAATACACTGCACATTGGAAACACAGAGTCAGCTACATTGCTGATTGTCCTCCGGGGCTTCCA  
GTTAAAGACTTGGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTGG  
CTTGACAAACTGAGGCAGTGAACACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTT  
GGATGCATTGGAGCATCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGA  
AGAAACTGCAACAATTGCAATTAAATACATCAAGCCTTTGTCGATTGCCAGCTAAATGGCTCCACAGTGG  
GTGGCGAAAACAACCTTCAGAGCTTGTAATGCCAGTTGTCGATGATTCTCCAGCTGCTAAAGGAAGAAGCAT  
TTTGCTGTTAGCCAGATGGCTTGTGATGATTCTCCAAACCCAGATCACGGTTCAGCCAGAAACAC  
AGTCGGCAATAAAAGGTTCCAATTGAGTTCTGCTGATGATTCTGCTCAGCTGCCAGCAGTGGATTCCCAATGACTTT  
GCTTGGAAAAAGAACATGAACACTGCACTGATGCTGAAATGGAAAATTATGCAACACCTCCGGGCAAGGTGG  
CGAGGTGATGGAGTACCCACATCTTCCGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTG  
TCATCTCAATCACTTGGTCATCCTACTCTGTCACAGCTAACAGCTAACAGTAAATATGCTTCCCTCATTCA  
AAGACCCCATGGATCTCACCATCCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGTTGGGCACCCAGC  
CCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGACTTCCAGCTGCACTGGAGAGACGCATGATGATGC  
CCGAGGATGACGTGTTCTTATCGTGGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCAAGCTCAGAAC  
AGTGCAGGAAGTATTCACTGCAACTCTGACTGCTCTAGAAACACCATCATTTCGGGCCACTGTTGGA  
CCGAACTGTAACCAAGGGAGAAACAGCCGCTTACAGTCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAC  
GGACCAAAGATGATAGCCATTGGGTAACCGAGAGGCACCTTTTGAGCAGGCAATCAGCTGATTATT  
GTGGACTCAGATGTCAGTGATGCTGGAAATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGGAA  
CGTGCCTCAGTGTGATCCCACCTCAACCTGCACTCCCTCAGATGACAGCCCCATCGTAGACGATGACG  
GATGGGCCACTGTGGGTGTCGTGATCAGCCGTGGTTGCTGTTGGGCACGTCACTCGTGTGGGGTC  
ATCATATACCAACACAAGGCGGAGGAATGAAGAGATTGCACTTACCAACACAGATGAGACCAACTGCCAGCAGA  
TATTCCTAGTTATTGTCATCTCAGGGAACGTTAGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAA  
GCCACCACCACTTGTACATCTCAGGTGCTGGATTTCCTTACACACATGACAGTAGTGGGACCTGCCAT  
ATTGACAATAGCAGTGAAGCTGATGTGAAAGCTGCCACAGATCTGTTCTTGTGCTGGGATCCACAGG  
CCCTATGATTGAAGGAAATGTGATGGCTCAGATCCTTGAACATACAGGTTGCACTGCTCAG  
CAAGAACAGTTTAATGGACCAACTGAGCCCACTGATGAAACATGAGGAAAGGAGCTACCCATGTTCTCATCCT  
TCAGAAGAACCTCGGAACGGAGCTCAGTAATATGTCAGGCTTACATGAGGAAAGCTACTTAACACTAG  
TTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTGTCACAAAGCTCCTTGTGAGGAAAGCT  
CAGAGCCAGCGTGGCTCGAGTAATTCTCATGGGTACCTTGAAAGCTCATTCTCC  
AGACTGGACTCTGGTCAGAGGAAGATGGGAAAGAAAGGACAGATTTCAGGAAGAAAATCACATTGAC  
TTAACACAGTTAGAAAACACTACAGGACTCCAATTTCAGTCTTATGACTTGGACACATAGACTGAATGAGAC  
CAAAGGAAAAGCTAACATAACTACCTCAAGTGAACCTTATTAAAAGAGAGAGAAATCTTATGTTTAAATG  
GAGTTATGAATTAAAAGGATAAAAATGTTTATTATACAGATGAACCAAATACAAAAGTTATGAAAAT  
TTTATGAGGAAATGATGCTCATATAAGAACATCCTTTAAACTATTGTTTATGCAAAAG  
TATCTTACGTAAATTAAATGATATAATCATGATTATTGTTATGTTTATAATGCCAGATTCTTTTATGGA  
AAATGAGTTACTAAAGCATTTAAATAACCTGCTTGTACCATTTTAAATAGAAGTTACTTCATTATATT  
TTGCACATTATATTAAATAAAATGTGTCAATTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN  
ITLLSLAGNRIEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLQLQHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSELDLTFNHLSRLDDSSFLGLSLLNLHIGNNRVSYIADCAFRLSSLKTLIDLKNNE  
ISWTIEDMNGAFSGLDKLRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSLLCDCQLKWLQPQWVAENNQSFVNASCAPHQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVIISNHFGSSYSVAKLTNVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQN  
SAGSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPLVVTER  
HFFAAGNQLLIVDSDVSDAGKYTCEMSNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLLDDG  
WATVGVIIIAVVCCVVGTSLVVVVIIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD  
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKCEYPCSHPSEESCRSFNISW  
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDKERTDFQEENHICTFKQTLENYRTPNFQS  
YDLDT

**Signal sequence:**

amino acids 1-19

**Transmembrane domain:**

amino acids 746-765

**N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

**N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459,  
528-534, 612-618, 623-629, 714-720, 873-879

## **FIGURE 103**

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPLSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNCIDL  
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN  
TTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN  
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS  
VHEPLLIRMNNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

## FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCACTGGAGTCTTTCGGTTTCCCTCCTGCTGTTGGGGGC  
ATGAAAGGGCTTCGCCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCAGCGAC  
GCGAGGGCGGGCGTCACCCCTCGGCTGGAAGTTGTGCCGGCCCCGAGCGCAGGGCTGGAGCTCGGT  
AGAGACCTAGGCCGCTGGACCGCAGAGCGCGCCAGCCTCCGTGCGCGCAGGGCTGGAGCTCGGT  
GTGCGCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGGGCTGCGGGAACTCGGGCAGCCCTCGGGTAG  
CCGCCGAGCGCCCATGCCCACTACCTGCCGCTGCCCTGGGACCTGCTGGACTGCAAGCGCTAGCG  
CGTCTTCCCGAGCCACTCCGTCCTGGTCGCTGGACTTAAGTCACAACAGATTATCTTCATCAAGGC  
AAGTCCATGAGCCACCTCAAAGCCTCGAGAAGTGAACAAACAATGAATTGGAGACCATTCAAATC  
TGGGACCAAGTCTCGGCAAATATTACACTTCTCCTTGGCTGAAACAGGATTGTTGAAATACCCCTGAACAT  
CTGAAAGAGTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCAAACACTGCA  
AGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTGACAATT  
TGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTAAACTG  
CCCCAACTGCAACATCTCGAATTGAACCGAAACAAAGATTAAAAATGTAGATGGACTGACATTCAAGGCCTTGG  
TGCTCTGAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCA  
ACATGGAATTTGAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGCTTACGGCTTGATG  
CTGCAGGAACCTCATCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCT  
CAGTGAGCTGGACCTAACCTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTGGCTAAGCTTACTAA  
ATACACTGCACATTGGAAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAG  
ACTTTGGATCTGAAGAACAAATGAAATTCCCTGGACTATTGAAGACATGAATGGTCTTCTGGCTTGACAA  
ACTGAGGGGACTGATACTCAAGGAATCGGATCCGGTCTTACTAAAGGCTTCACTGGTTGGATG  
TGGAGCATCTAGACCTGGATGACAACGCAATCATGCTTCTAACAGGCAATGCATTTCACAAATGAAGAAACTG  
CAACAAATTGCAATTAAACATCAACGCTTGTGCCAGCTAAAGGCTCCCACAGTGGTGGCG  
AAACAACTTCAGAGCTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAAGCATTGCTG  
TTAGCCCAGATGGCTTGTGATGATTTCACAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCA  
ATAAAAGGTTCCAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGATTCCCCAATGACTTTGCTTGGAA  
AAAAGACAATGAACTACTGCATGATGCTGAAATGAAAATTATGCACACCTCCGGCCAAGGGTGGCGAGGTGA  
TGGAGTATACCACCATCCTCGGCTGCCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCC  
AATCACTTTGGTCATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCC  
CATGGATCTCACCATCCGAGCTGGGCCATGGCACGCTGGAGTGTGCTGTGGGGCACCCAGCCCCCAGA  
TAGCCTGGCAGAAGGATGGGGCACAGACTTCCAGCTGCACGGAGAGACGCATGTGATGCCAGGG  
GACGTGTTCTTATCGTGGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGG  
AAATTTCAAGCAATGCAACTGACTGTCTAGAAACACCACATTTCGCCACTGTTGGACCGAAC  
TAACCAAGGGAGAAACAGCGCTTACAGTCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAA  
GATGATAGCCCATTGGTGGTAACCGAGAGGCACTTTTGCACTGGCAATCAGCTTCTGATTATTGTGACTC  
AGATGTCAGTGATGCTGGAAATACACATGTGAGATGTCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCC  
TCAGTGTGATCCCCACTCCAACCTGCAGCTCCCTCAGATGACAGCCCCATGTTAGACGATGACGGATGGGCC  
ACTGTGGGTGCTGATCATGCCGTGTTGCTGTGCTGGCAGCTCACTCGTGTGGGTGGTCATCATATA  
CCACACAAAGGGGAGGAATGAAGATTGCACTTACCAACACAGATGAGACCAACTTGCAGCAGGATATTCC  
GTTATTGTCATCTCAGGGAAACGTTAGCTGACAGGGCAGGATGGGTACGTTCTCAGAAAGTGGAAAGCCACCAC  
CAGTTGTCACATCTCAGGTGCTGGATTTCACACATGACAGTGGACCTGCTGATGAGGAAAG  
TAGCAGTGAAGCTGATGTTGGAGCTGCCACAGATCTGTTCTTGTCCCTTTGGGATCACAGGCCCTATGT  
ATTGAAAGGGAAATGTGATGCTCAGATCCTTGGAAACATATCATACTGAGGTTGCACTGCTGACCC  
GTTTAATGGACCACTATGAGGCCAGTTACATAAAAGAAAAGGAGTGCTACCCATGTTCTCATCCTCAGAAGA  
ATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCTTACATGAGGAAAGCTACTAACACTAGTTACTCTC  
ACAATGAAGGACCTGGAATGAAAATCTGTGCTAAACAAGTCCCTTGTGAAATTTAGTGC  
GGCTGGGTGCTCGAGTAATTCTTCATGGGACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGC  
TTCAAGCTTGGACAGCCATCAGATTGTCAGCCAAGAGCCTTTATTGAAAGCTCATTCTCCAGACTGG  
ACTCTGGGTGAGGGAAAGATGGAAAGAAAAGGACAGATTTCAGGAAGAAAATCACATTGTA  
ACTTTAGAAAACACAGGACTCCAATTTCAGTCTTATGACTGGACACATAGACTGAATGAGACCAAGGAA  
AAGCTTAACATACTACCTCAAGTGAACCTTATTAAAGAGAGAATCTTATGTTTTAAATGGAGTTATG  
AATTGAAAGGATAAAATGTTATTATACAGATGAACCAAATTACAAAAGTTATGAAAATTTTATAC  
TGGGAATGATGCTCATATAAGAATACCTTTAAACTATTGTTATGCAAAAAGTATCTTAC  
GTAAATTAAATGATATAATCATGATTATTGTTATGATTGTTATAATGCCAGATTCTTATGAAAATGAGT  
TACTAAAGCATTAAATAATACCTGCCCTGTACCATTTTAAATAGAAGTTACTTCATTATATTGAC  
TATATTAAATAAAATGTCATTGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMGAFWGGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSLDLTFNHLSSLRDLSSFLGLSLLNTHIGNNRVSYIADCAFRLGSSLKTLDLKNNEIS  
WTIEDMNAGAFSGLDKLRRRLLQGNRIRSIKKAFGLDALEHLDLSDNAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWLQPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPQLNWTKDDSPLVVTERHF  
FAAGNQLLIVDSDVSDAGKYTCMSNTLGETGNVRLSVIPTPTCSPQMTAPSLLDDGWA  
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPTYLSSQGTLADRO  
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGPMY  
LKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCSHPESESCERSFSNISWPS  
HVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYD  
LDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473,  
515-519, 688-692, 729-733, 905-909, 987-991, 999-1003,  
1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328,  
374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713,  
731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007,  
1018-1022, 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

## **FIGURE 108**

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPPEENEFAEEEPLVLSPEEPGPGPAAVSCPRDCACSQEGVVDGGIDLREFPGDLP  
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFFEHTNLNYLYLANNK  
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPVRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEETR

**Signal sequence:**

amino acids 1-48

**N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

**Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

**N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242,  
335-341, 477-483, 498-502, 539-545, 548-554

**Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486,  
471-493, 535-557

## **FIGURE 109**

GGGAGGGGGCTCCGGCGCCGCGCAGCAGACCTGCTCCGGCGCGCCCTGCCGCTGTCCTCCGGGAGCGGCA  
GCAGTAGCCCGGGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCTCCCCTCGCGCCACAC  
CCCAACCTGTTCTCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTTCCTCGCGCT  
GGTGTGGTATCTCGCTCACCTGCGAGGCGCCGAGTCAGCAGGGAGGTGGCCAGGCAAATAGTGTCT  
CGATTGGCCTATGTCGTTATGGTGGAGGATTGACTGCTGCTGGGGCTGGCTGCCAGTCTGGGACAGTGT  
CAGCCTGTGCAACCACGATGCAAACATGGTGAATGTATCGGGCAAACAAGTCAAGTGTCTGGTTA  
TGCTGGAAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGATGA  
ACACTTACGGCAGCTACAAGTGTACTGCTCAACGGATATATGCTCATGCCGGATGGTCTGCTCAAGTGCC  
CTGACCTGCTCCATGGCAAACACTGTCAGTATGGCTGTGATGTTAAAGGACAAATACGGTGCCAGTGCCCATC  
CCCTGGCCTGCACCTGGCTCTGATGGAGGACCTGTGAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCT  
GCCCTAGATTAGGCAATGTGCAACACTTGGAGCTACATCTGCAAGTGTCTAAAGGCTCGATCTCATG  
TATATTGGAGGCAAATATCAATGTATGACATAGACGAATGTCACCTGGTCACTGTCAGTATCAGTGCAGCAGCTTG  
TCGATGTTATAACGTACGTGGTCTACAAGTGCACATGTCAGTAAAGAAGGATACAGGGTGTGACTGACTTGT  
TGTATATCCAAAAGTTATGATTGAAACCTTCAGGTCATTGTCACAAAGGAAATGGTACCTTAAAG  
GGTGACACAGGAAATAATAATTGGATTCTGATGTTGAAAGTACTTGGTGGCCTCCGAAGACACCATATATTCC  
TCCTATCATTACCAACAGGCCACTTCTAACGCAACACAAGACCTACACCAAGCCAACACCAATTCTACTC  
CACCACCACCAACCCCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCAACCACC  
GGACTGACAACATAGCACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGA  
CCCTCAGAAACCCAGAGGAGATGTGTTCACTGTTCTGGTACACAGTTGTAATTGGACCATGGACTTTGTGGAT  
GGATCAGGGAGAAAGACAATGACTGCACTGGAAACCAATCAGGGACCCAGCAGGGACAATATCTGACAGTG  
TCGGCAGCAAAGCCCCAGGGGAAAGCTGCACGCTTGGCTACCTCTGGCCCTCATGCAATTGAGGG  
CCTGTGCTGTCACTCAGGCAACAGGTGACGGGGCTGCACTTGGCACACTCCAGGTGTTGAGAAAACACG  
GTGCCCACGGAGCAGCCCTGTTGGGAAAGAAATGGTGGCCATTGGCTGGAGGGCAAACACAGATCACCTGCGAGGG  
GCTGACATCAAGAGCGAACATCAAAGATGATTAAGGGTTGGAAAAAAAGATCTATGTTGAAATTAAGGAA  
CTGGGATTATTGAGCTGGAGAAGAGAAAGACTGAGGGGAAACCCATTGATGTTCAAGTATATGAAGGGTTG  
GCACAGAGGGTGGCAGGACTGTTCTCCATTGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAG  
AGTATAAGGGAGCATTCTGGCAGGGCCATTGTTAGAATACTTCATAAAAAAGAAGTGTGAAATCTCAGT  
ATCTCTCTCTTCTAAAAATTAGATAAAATTGTCTATTAGTAAAGATGGTAAAGATGTTCTACCAAGGA  
AAAGTAACAAATTAGAATTCCAAAAGATGTTGATCCTACTAGTAGTATGCACTGAAATCTTAAAC  
TAAATAATTGGACAAGGCTTAATTAGGCATTCCCTCTGACCTCTTAATGGAGAGGGATGAAAGGGAAAG  
AGCCCACCAATGCTGAGCTCACTGAAATATCTCCCTTATGCACTTGGAGTATTAAAGAAAAAGGAA  
ACTATTATTCCAAATGAGAGTATGATGGACAGATATTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGT  
TTCAATGTTCTTCATGGTAAAGGTATAAGCCTTCATTGTCATGGATGATGTTCAGATTTTTTT  
TAAGAGATCCTCAAGGAACACAGTTCAGAGAGATTTCATGGGTGCAATTCTCTGCTTGTGACAAG  
TTATCTGGCTGCTGAGAAAGAGTGCCTGCCACACGGCAGACCTTCTTCACCTCATCAGTATGATTCA  
GTTTCTCTTATCAATTGGACTCTCCAGGTTCCACAGAACAGTAATATTGAAACAATAGTACAATAGAAG  
GTCTCTGTCATTAACTGGTAAAGGCAGGGCTGGAGGGAAAATAATCATTAGCCTTGAGTAAAGGCA  
GAATATATGGCTGAGATCCATTGTTAATGGTCAATTCTTATGGTCATATAACTGCACAGCTGAAGATGAA  
AGGGAAAATAATGAAAATTACTTTGCACTGCAATGATACATTGCACTAAACTGATGAAAGAAGTATCC  
AAAGTACTGTATAACATCTGTTATTATTTAATGTTCTAAATAAAATGTTAGTGTGGTTCTCAAATGGC  
CTAATAAAAACAATTGTAATAAAAACACTGTTAGTAAT

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCOPVCQP  
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRCPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRCTVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN  
RVQTDPQKPRGDVFSLVHSCNFHDGLCGWIREKDNDLHWEPIRDPAQQYLTVSAAKAPGG  
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 273-277

**Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

**Tyrosine kinase phosphorylation site.**

amino acids 199-206

**N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227,  
236-242, 421-427, 433-439, 462-468, 476-482

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

**Cell attachment sequence.**

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACCTTCCTTGCACAGGTGCTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA  
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGAATACC  
AACACAAGTTACCATGATGCCACCCATGCATCTGCTTATCAACCCACTGCAGTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACCTCTATGCCAGTCA  
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGACATGACCTGACATGCCATGTGAAGGGGGACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC  
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCGTCACTGAAATGAAAGTGAATATTATGCCATCATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGCCTCGCTAGAAGTT  
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGTGTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTACAGTTATCATCACTCCGTAGGACTGGAGAACGTTG  
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTGGATT  
ATATCCATGTGTTCTCTTCTATGGAAAAAAATATCAACCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAACAGAAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG  
CTCTGGATGACTCGGAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGGCAAGATTGACAGTACAGT  
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTATGG  
GCTAAACAGTACATTGAGTGAATTCTGAAGAACATTAAAGGAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCTTACA  
TGCAGAATAGAGGCATTATGCAAATTGAACTGCAGGTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGTTCTCTCATAGTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTTTATTAGTG  
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTGTTATTGTACAA  
CAAAGTAATAAGGATGGTGTCAAAAAACAAAACATGCCTCTCTTTTCAATCACC  
AGTAGTATTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA  
TTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGCTTTAAAAAA  
AA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPIVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV  
DLGEAIFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

**Signal sequence:**

amino acids 1-18

**Transmembrane domain:**

amino acids 341-359

**N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

**Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430,  
433-437

**Tyrosine kinase phosphorylation site.**

amino acids 272-280

**N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## **FIGURE 113**

GCAAGCGGC~~GAA~~ATGGCGCCCTCCGGGAGTCTGCAGTCCCTGGCAGTCCTGGTGTGTT  
GCTTGGGGTGCTCCCTGGACGCACGGGCGGCGAGCAACGTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCCGTGGTGCCTGCT  
TGTCAAAATCTCAACCGGAATGGGAAAGTTTGTGAATGGGGAGAAGATCTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC  
TTCCTACTATTATCATTGAAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAACTTATAAGTGATAAAGAGTGGAAAGAGTATTGAGCCCGTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTATTGAAAGACCTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC  
AGATTGCCTTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT  
TATTATCAGAACTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCCATGAAGAA  
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAACATGC  
CATAAGACAACGCTCTGGTCCATCATGGCCACAGATAAAATCCTAGTTAAATTTATAG  
TTATCTTAATATTGATTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG  
AACTGTGACTTTTGAATATTGAGGGTTCAGTCTAGATTGTCATTAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG  
GTTTAATAGTTCTCTAATTTGAAAAACGTGCCAAGCAATAAGATTATGTATATTGT  
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT  
TGAGGTATTAAAGAAGATTATTAGAGAAAATATTCTCATTTGATATAATTCTCTG  
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG  
AAATGTGTATTCAGTGACAATTCTGTTCTTGTAGAGGTATATTCAAATTCCTGT  
ATTTTAGGTTATGCAACTAATAAAACTACCTACATTAATTACAGTTCTACACA  
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATTC  
CAACAAAGTTGATTTCTCTGTTACTTACTATGGTTACATTTTATTGTT  
CAAATTGGATGATAATTCTGGAAACATTTTATGTTAGTAAACAGTATTGTTGTT  
GTTTCAAACTGAAGTTACTGAGAGATCCATCAAATTGAAACATCTGTTGTAATTAAAATT  
TTGGCCACTTTTCAGATTTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTTT  
TTTCTTTGGATGTGAAGGTGAACATTCTGATTGTTGCTGATGTGAAAAAGCCTGGTA  
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCAATTCTACTCAGGAAAAG  
CATCTTCTGTATATGCTTAAATGTTGCTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTGATTTAAAATAACATTATTTTATATTGTTAAAGACAA  
ACTTCATATTATCCTGTTCTCCTGACTGGTAATTGTTGTTGAGGATTCACAGGAAAAA  
GTCAGTAGGATGGAACATTTAGTGTTACTCCTTAAAGAGCTAGAACATACAGTTT  
CACCTTAAAGAAGGGGAAAATCATAAAACAAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGCCCCCTCTTCTAGGCTCTGCTGCTGTAATCCATTAGATTACAG  
TATCGTAATATAACAGTTCTTAAAGCCCTCTCCTTAGAATTAAATATTGTA  
AAAGAGTTGGATGTGTAATTGATGCCATTAGAAAAATATCCTAACGACAAAATAACCT  
TTCTAACCACTCATTAAAGCTGAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL  
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 182-201

**Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

**Tyrosine kinase phosphorylation site.**

amino acids 107-115

**N-myristoylation site.**

amino acids 20-26, 192-198

**Amidation site.**

amino acids 25-29

## **FIGURE 115**

GCAGTGTCCAGCTGCGGAGACCGTATAATTGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCGAGTGGACAGGCGGATTGGAAGAGCGGG  
AAGTCCTGGCCAGAGCAGTGTGACACTCCCTCTGTGACC**ATGAAACTCTGGGTGTCTGC**  
ATTGCTGATGGCCTGGTTGGTGCCTGAGCTGTGACAGGCCAATTCTTACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTGTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCTGCGCTGGAGGACCTGTGCTGCAGGACTCAGCTGCA  
GGTTTATGCCAACCTCTGTGAGCAGCTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA  
GAGGGAACTTCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG  
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTTGGATGGAGCAGGTGCT  
AAAGCAGCTGATGCCGGGAGGAGGCCACACAAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTCCAGTTGGTGTCTGCACCGTGCCTGGAGCTCACCCGCCCTGCTC  
TCCCTGACCAAGCCACGAACGAGCTGGAGGAACTGCGGTACTTGTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA  
TCTATGAGAGGCCTGTGACTACCTGCCTGAGAGGGATGTTACGAGAGCCTCTGTGCTGG  
GAGGGTGTCAAACACTGACACCCGTAGACAGAAAGAGGCTTTCTGTAGGTACCAATGGCAA  
CAGGGCCCACAGCTGCTCATTGCCCTCAAAAGAGGAGGACGAGTGGACAGCCGCACA  
TCGTCAGGTACTACGATGTCATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGAAAAA  
CCTAAACTTGACGAGCCACCGTCTGATCCAAAGACAGGAGTCCTCACTGTCGCCAGCTA  
CCGGTTTCCAAAAGCTCTGGTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAAGATTGTTACAGGTTGCAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCATTGACTTCTCTAGGCGACCTTGACAGCGG  
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG  
GTGGTGCCACCGTCTCCCTGATCTGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCC  
TGTGCTTGTGGCTGCAAGTGGCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAACAGTTGACTGACATCCTTCTGTCTCCCTGGTC  
CTTCAGCCATGTCACAGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT  
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATTGAGCCTGTGCCATCCCTGGCCCAAGGCTAGGATCA  
AAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCTAGCAAGGTGCCTTGTACCTCAGGTT  
TTAGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT  
GGCATTCTATCTATTGTGGTTACCAAAAATAAAATGCCCCTACCAAGAAAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWALEDLVLQDSAAGFIANLSVQRQFP  
TDEDEIGAAKALMRLQDTYRLDPGTISRGELOPGTYQAMLSVDDCFGMGRSAYNEGDDYYHTV  
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTTRRLSLDPHSERAGGNLR  
YFEQLLEEREKLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEGVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIYRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

## **FIGURE 117**

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTG  
TTTCATTATTACCGTTTGGCTGGGGTTAGTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGT  
GAAGACAGGACAATCTTCTGGGATGCTGGCTGGAAAGCCACGGGCTTGCCTGTCTTGGCCTCATTGA  
CCCCAGGTTCTGGTTAAACTGAAAGCTACTACTGGCCTGGTCCCCTAATCATTGATCCTGAGGCTG  
TGCCCCCTGGGACCCACCTGGCAGGGCTTACCAACCATATGCGACTGAGCTCCCTGTTGGCTCTGCTGCCAGC  
GCTTCCCCCATCTTAGGGCTGCTCTGGGTGAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGG  
GAGAAGATCCCTGTCAGGGTGTAGGGAGCAGGGAGGACAGAACTCAGATTGAGAGCTCGGCTAGAC  
CAAAGTGTGAAGACTCAAACCCGGATTGTCCCCACTACAGGGACCCAAACAGCCCTACAAGAAGGTGT  
CAGGACTCGGTACATCCAGACAGAGCTGGCTCCCGTGAGCGTTGCTGGCTGTCTGACCTCCGAGCTA  
CACTGTCCACTTGGCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTGGTTACTCTACTTCAGTGG  
CAGCGGGGGGCCGGCTCCAGCAGGGATGCGAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTATGTC  
AGAGACCTCGGCCACCTCACACACACTTGGGGCGACTACGACTGGTCTTCATCATGCAAGGATGACACAT  
ATGTGCAGGCCCGCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCA  
GAGGAGTTCATGGCGCAGGCAGCAGGGCCGGTACTGTATGGGGCTTGGCTACCTGTTGTCACGGAGTCT  
CCTGCTCGTCTGCGGCCACATCTGGATGGCTGCCAGGAGACATTCTAGTGCCGCTGACGAGTGGCTTG  
GACGCTGCCATTGACTCTGGCGTGGCTGTCTCACAGCACCAGGGCAGCAGTATCGCTATTGAA  
CTGGCCAAAATAGGGACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCGCCGTGACCCCTGCTC  
CGAAGGTACCCATGTACCGGCTCCACAAACGCTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAG  
AAACAATGCAAGGCTCAGATCCGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTT  
GGGCTCCCTGCTCCCTTACACCAACTCTCGCTTGAGGTGCTGGACTACTTCACAGAGCAGCACAC  
CTTCTCGTGCAGATGGGCTCCAAGTGCCTACAGGGGCTAGCAGGGCGACGTGGTGTGCTTGG  
AGACTGCCCTGGAGCAGCTCAATGGCGCTATCAGCCCCGCCCTGCGCTTCCAGAAGCAGCGACTGCTCAAGCC  
TATCGCGCTTCGACCCAGCACGGGAGCTGGAGTACACCTGGACCTGCTGTTGAAATGTTGACACAGCGTGG  
GCACCGGGGGGGCTGGCTGGCAGGGCTGGCTGGCTGAGGCTTCCAGGTGCGACTCATGGACGTGGTC  
ATGTCACTGAGGCCACCGAGTGCAGCTGGTGTGCCACTCTTGGCTGAAGCTGCTGCAGCCCCGGCTTTC  
CTCGAGGCCTTGAGCCAATGTCTGGAGCCACGAGAACATGCAATTGCTCACCTGTTGCTGGCTACGGGCC  
ACGAGAAGGTGGCGTGGAGCTCCAGACCAATTCTGGGGTGAAGGCTGCGAGCGAGGTAGAGCAGGGT  
ACCCCTGGAGCAGGGTGGCTGGCTGGCTGAGGCTTCCAGGTGCGACTCATGGACGTGGTC  
TCGAAGAACGCCCTGAGCAGCTCTTCTTACCAACCGTGTGGACAAGGCCCTGGGCCAGTCTCAA  
CCGCTGTCGATGAATGCCATCTCTGGCTGGCAGGCCCTTCCAGTCCATTCCAGGAGTCAATCCTGCC  
TGTCAACACAGAGATCACCCCCAGGGCCCCGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCC  
TCCCAGGGGGCTCTATAGGGGGAGATTGACGGCAGGCTTCTGGGAGGGCTGCTTCTACAACGCTGACTA  
CCTGGCGCCCGAGGCCGGCTGGCAGGTGAACGGCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGG  
TGATGGATGTTCTCCGGTCTCAGGGCTCCACCTCTTCCGGCGTAGAGCCAGGGCTGGTGCAGAAGTTC  
TCCCTGCGAGACTGCAGGCCACGGCTCAGTGAAGAACTTACCAACGCTGCCGCTCAGCAACCTGGAGGGCT  
AGGGGCCGTGCCAGCTGGCTATGGCTCTTTGAGCAGGAGCAGGCCAATAGCACTATGCCGCTGGGGC  
CCTAACCTCATTACCTTCTTGTCTGCCAGCCCCAGGAAGGGCAAGGCAAGATGGGACAGAAGAGAA  
TTGTTGCTGTATTTTAAATGAAATGTTATTAAACATGCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDZRARLD  
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY  
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSRLLLRLRPHLDGCRG  
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR  
RFDPARGMEYTL DLL LECVTQRGHRRALARRVSLLRPLS RVEILPMPYVTEATRVQLVLPPLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG  
TRLAWLAVRAEAPSQVRLMDVVKHPVDTLFFLTTVWTRPGPEVLRNCRMNAISGWQAFFP  
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNA  
RARLAGELAGQEEEAELEGLEVMDVFLRFSGHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRQLAMALFEQEANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372,  
385-389, 399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## **FIGURE 119**

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGC CGC GGCTGC GCTT CCTGTCCC AAGCC  
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG  
AAGCATTTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC  
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACCAAACACTGTGACAAAGCAG  
AGTTCTCAGTCTGAAAATGTTAAAGTGTGAGTCAATTAAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTGATAAGTATAGAGACCAATACA  
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA  
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTGAA  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCT  
CAATATCCCAGAAAAGTGCCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATA  
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCA  
AAAGATGTATTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC  
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACT  
ATCAGATGCATGTGATGTATGGGTATACCGCCTAGGGCATTGGCATATTTCAAT  
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAGCG  
TGAATATGATCTTGTATAGGACGTGTGTCATTATTTGTTAGTACTACATA  
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTAAATGAGGGGGTTTTCTTAAAACACATGAACATTGAA  
TGTTGGAAAGAAGTTTAAGAATAATAATTGCAAATAAAACTATTAATAAATATTAT  
GTGATAAATTCTAAATTGAAACATTAGAAATCTGTGGGCACATATTTGCTGATTGGTT  
AAAAAAATTAAACAGGTCTTAGCGTTCTAACAGATATGCAAATGATATCTCTAGTGTGA  
TGTGATTAAAGTAAAACTTAGCTGTGTCCCTTACTCTAACACTGATTATGTTCT  
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACA  
ATTAAAGTGA  
AAAGTTGAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

**Signal sequence:**

amino acids 1-33

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372,  
385-389, 399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

## FIGURE 121

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSCYNYGSSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGS

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTGACATGGCGCTGAGGC GGCCACCGCGA  
CTCCGGCTCTGCGCTCGGCTGACTCTTCCCTGCTGCTGCTTTCAAGGGCTGCCTGATAGGGCTGTA  
TCTCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATT  
CGCAGACAAGTGAACCCAGGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACA  
AAAATTCAAGGGAGACTTGGCGGGCTGTCAGAAATACTGGGAAGACATCCCTGAAAGATCTGAAATGTGACACG  
GAGAGACTCAGCCCTTATCGCTGTGAGGTCGTTGCTCGAAATGACCGAAGGAATTGATGAGATTGTGATCG  
AGTTAACGTGCAAGTGAAGCCAGTGAACCCCTGTCGAGTGTAGAGTGCAGGCTGTACCGTAGGCAAGATGGCA  
ACACTGCAGTGCAGGAGAGTGAAGGGCACCCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCACTGCC  
CACGGATTCCAGAGCCAATCCCAGATTTCGCAATTCTTCCACTTAAACTCTGAAACAGGCACCTTGGTGT  
TCACTGCTGTTCACAAAGGACGACTCTGGCAGTACTACTGCATTGCTTCAATGACCGCAGGCTCAGCCAGGTGT  
GAGGAGCAGGAGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGCTGGTGTCTGCTGT  
ACTGGCCCTGATCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAG  
AAAGTTACAAGAACCCAGGGAAACCAAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGACTTCAGACAC  
AAAGTCATCGTTGTGATCTGAGACCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTGCTA  
GAAACTCCTGTCAGGCAAGCAGAGCTGATGCACTGGACAGAGCTAGACACTCATTAGAAGCTTCTGTTT  
GGCCAAAGTTGACCAACTACTCTTACTCTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCG  
GTAAATATAACCACAAGGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTAATCTGTTCTGGCTGATT  
CCCGCATGAGTATTAGGGTGTCTAAAGAGTTGCTCACGTAACAGCCCGTGTGGCCCTGTGAAGCCAGCA  
TGTTCACCACTGGTCGTTCAGCAGCCACAGCACCATGTGAGATGGCAGGTGGACAGCACGACAGC  
GCATCCGGCGGGAACCCAGAAAAGGCTTACACAGCAGCCTACTTCATCGGCCCACAGACACCACCGCAG  
TTTCTTCTAAAGGCTCTGCTGATCGGTGTTGAGTGTCCATTGTGGAGAAGCTTTGGATCAGCATTGTA  
AAAACAACAAAATCAGGAAGTAAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCCGCTGTCCAAC  
AGGGTGTCAAGGATTAAAGGAAACCTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGTTCTATGG  
GTCTGTTATTAAATTTACATCTAAATTGCTAAGGATGTTTGATTATTGAAAAGAAAATT  
CTATTAAACTGTAATATATTGTACATACAATGTTAAATAACCTATTTTAAAAAGTTCAACTTAAGGTAG  
AAAGTTCCAAGCTACTAGTGTAAATTGGAAAATATCAATAAACTTAAGAGTATTACCCAAAGGAATCCTCTCATG  
GAAGTTACTGTGATGTTCTTTCTCACACAAGTTAGCCTTTACAAGGGAACTCATACTGTCTACACA  
TCAGACCATAGTGTGTTAGGAAACCTTAAATCCAGTTAAAGCAATGTTGAAATCAGTTGCTATCTTCAA  
AAGAACCCCTCAGATGTACATACACAGATGCCAGTCAGCTCTGGGTTGCCAGGGCCTAGCTCA  
CTGTTGCTCGCTGCTGCCAGGAGGCCCTGCCATCCTGGCCCTGGCAGTGGCTGTGCTCCAGTGA  
CTCACGTGGCCCTGCTTACAGCACAGCTCAGGTGGCACTGCAGGGACACTGGTGTCTTCCATGTAGC  
GTCCCAGCTTGGCTCTGTAACAGACCTCTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTA  
TTTTTTTTAAAGTTGTTAATTATTGTTAAAGATTGCTAAGGCCAAAGCAATTGCGAAATCAAGTCTG  
TCAACTACAATAACATTAAAGAAAATGGATCCACTGTTCTCTTGCACAGAGAAAGCACCCAGACGC  
CACAGGCTCTGTCGCAATTCAAAACAAACCATGATGGAGTGGCAGGCCAGCTTAAAGAACGTCAGGT  
GGAGCAGCCAGGTGAAAGGCCCTGGCGGGAGGAAGTGAACACGCCGATCAAAAGCAGTTCTAATTGAC  
TTAAATTTCTCCGCGGAGACACTGCTCCATTGTGGGGGACATTAGCAACATCACTCAGAACGCTGT  
GTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCTGCCGCTGGACTCAGGACTGAAGTGTGTA  
AGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCGGAGAATGGCTCTACTACTCACCTGTCTCAGCTT  
CCAGTGTCTGGTTTTTAACTTGTACAGCTTTTTAATTGCTACATGAGACTGTGTTGACTTTTTA  
GTTATGTGAAACACTTTGCCGAGGCCCTGGCAGAGGCAGGAATGCTCCAGCAGTGGCTCAGTGTCTCC  
GTGCTGCTGCACTGGCATCTGGATGCTTAGCATGCAAGTTCCCTCCATCATTGCAACCTGGTAGAGAGGGAT  
GGCTCCCCACCCCTCAGCGTTGGGATTCACTGCTCCAGCCTCTTGTGTTGCTAGTGAAGGGTACGCC  
TTGCCCTCTCTTCTTAAACCTTCAACTAGTGCCTGGGACATGGGAAACAGGCTGAAAGAAGAGA  
GTGAAAGTAGAGTCTGGGAAGTAGCTGCCCTAAACTGAGACTAGACGGAAAAGGAATACTCGTGTATT  
TATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCTGCCCTGGATGGATGGTGTACACAG  
ATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAACCTCATTATAAAAGCTTCAAAAAAC  
CA

## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFL~~LLL~~FRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD  
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS~~L~~KIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVT~~P~~VCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG  
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267